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Compugen Ltd.
GenCore version
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OM protein - protein search, using sw model

Run on:

January 11, 2006, 15:07:51; Search time 77 Seconds (without alignments) 992.882 Million cell updates/sec

US-10-650-123-2 868 1 MKKALATLIALALPAAALAE.......VNIVKNVRSGELSVGVRVKF 174 Title: Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2443163 segs, 439378781 residues Searched: Total number of hits satisfying chosen parameters:

2443163

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_21:\* Database :

geneseqp1980s:\*
geneseqp1990s:\*
geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2001s:\*
geneseqp2003as:\*
geneseqp2003as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aaw04891 Proteinas	Abu79079 N. mening	Adf43316 N. mening		Adl13428 Neisseria	Adl24352 N meningi	Aea03010 Neisseria	Adp08236 Neisseria	Aeb93444 Neisseria	Adl24383 N meningi	Aaw04893 Proteinas	Aaw04894 Proteinas	Abg91063 Neisseria	Aaw04892 Proteinas	Adl24385 N meningi	Abp77991 N. gonorr	Adl24387 N meningi	Adl24386 N meningi	Aab19895 Neisseria	Š	Adl24384 N meningi	Adl24388 N meningi	Adl24389 N meningi	Aao17579 M catarrh
SUMMARIES		ΩI	AAW04891	ABU79079	ADF43316	ADL16114	ADL13428	ADL24352	AEA03010	ADP08236	AEB93444	ADL24383	AAW04893	AAW04894	ABG91063	AAW04892	ADL24385	ABP77991	ADL24387	ADL24386	AAB19895	ADL13426	ADL24384	ADL24388	ADL24389	AA017579
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# ALIGNMENTS

RESULT 1

AAW04891 standard; protein; 174 AA. 16-OCT-2003 (revised) 22-DEC-1996 (first entry) AAW04891; AAW04891 AAW048

Proteinase K resistant N. meningitidis 22 kD surface protein.

Proteinase K reistant; Neisseria meningitidis; Neisseria gonorrhoeae; antibody; detection; probe; surface protein.

Neisseria meningitidis; strain 608B.

Location/Qualifiers Peptide Protein

1. .19 /label= sig\_peptide 20. .174 /label= mat\_protein

(2)60)

96WO-CA000157. 15-MAR-1996; 26-SEP-1996.

18-31-90360W

Hamel J, Rioux C; (IAFB-) IAF BIO VAC INC. Brodeur BR, Martin D,

95US-00406362. 95US-0001983P.

17-MAR-1995; 04-AUG-1995;

WPI; 1996-443187/44. N-PSDB; AAT39039.

Neisseria meningitidis antigen, highly conserved between different strains - useful for prodn. of antibodies for immunisation against, or diagnosis of, N. meningitidis infection.

Claim 7; Fig 1; 117pp; English.

A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen, antigenic fragments of antibodies can be used in a vaccine for the

sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,

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             humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen. DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                PAVDYTRYKNYKAPSTDFKLYSIGASAIYDPDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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gonorrhoeae in
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                                                                                                                                                                Length 174;
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meningitidis or by N.
                                                                                                                                                                100.0%; Score 868; DB 2;
100.0%; Pred. No. 1.1e-86;
ive 0; Mismatches 0;
prevention of infection by N.
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ABU79079 standard; protein; 174 AA (first entry) 18-JUN-2003 ABU79079; RESULT 2 ABU79079 

N. meningitidis lipopolysaccharide protein.

Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis; gene therapy; mammalian cell receptor; cytostatic; tumour associated lipid; anergy; T cell; antigen presenting cell; APC; tumouricidal immunocyte; antitumour.

Neiserria meningitidis.

US2002177551-A1.

28-NOV-2602.

30-MAY-2001; 2001US-00870759.

31-MAY-2000; 2000US-0208128P

(TERM/) TERMAN D S.

Terman DS;

WPI; 2003-361759/34. N-PSDB; ACA64711. A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis in T cells and antigen presenting cells.

Disclosure, Page, 167pp, English.

The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumour associated lipids and induces anergy or apoptosis in the T cells and antigen presenting cells (APCs). Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (MI) a tumouricidal immunocyte population in vivo in a mammal (by allowing tumour associated lipids to context immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycolipids,

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c sphingolipids, glycosphingolipids, phosphosphingolipids, gradialiosatdes, calalylated glycans, lipopeptides and proteoglycolipids are inactivated or deleted), a construct useful in the treatment of cancer comprising a superantigem (549) nucleotide inserted into a virus, a mammalian T cell canteriated in the treatment of cancer (where an adaptor protein which the present comprising a lipid raft conjugated antigens is deleted or inhibits T cell activated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producing (fX) a tumouricidal immunocyte population ex vivo in a mammal (by allowing tumour associated lipids are inactivated or deleted to produce a tumouricidal immunocytes to the host), producing the tumour cidal ApC contact ApCs, in which receptors for the tumour associated lipid to contact ApCs, in which receptors for the tumour associated lipid to contact ApCs, in which receptors for the tumour associated lipid to contact ApCs, in which receptors for the tumour associated lipid to contact ApCs, in which receptors for the tumour associated lipids to contact ApCs, in which adaptor proteins, which inhibit T cells and administering ApCs to the host), producing a tumour associated lipids to contact ApCs, in which adaptor proteins, which inhibit T cells, and administering the tumouricidally activated or functionally activated to produce a tumouricidal population of T cells, and administering the tumouricidally activated T cells to the host), treating cativated to produce a tumouricidal population of T cells to the host, treating that immunospressive tumouricidally activated T cells to the host, treating cumour associated lipid activated T cells to the host, a tumouricidal T cell population in vivo in a mammal (by allowing a cumouricidal T cell population in vivo in a mammal (by allowing a tumouricidal T cell activated and producing (minibit T cell activated on the mammal (by allowing a cumouricidal T cell activated by the mammal compositions are deleted or 
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100.0%; Pred. No. 1.1e-86;
tive 0; Mismatches 0;
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The invention relates to a process for producing an outer membrane vesicle (OMV) preparation from a bacterium. The process involves disrupting the bacterial membrane substantially in the absence of decorycholate detergent or other detergent, followed by several corritingation steps. Membrane disruption is achieveded by sonication, centrifugation steps. Membrane disruption is achieveded by sonication, homogenisation, microfluidisation, cavitation, osmocif shock, grinding, French press, belnding or any other physical technique. The outer membrane vesicles can be prepared from bacteria of the genera Moraxella, Shigella, Pseudomonas, Treponema, Porphyromonas, Helicobacter or Neisseria, and are particularly produced from Neisseria meningitidis (especially serogroup B) or Neisseria gonorrhoeae. The invention also relates to a Neisseria meningitidis outer membrane vesicle composition in which the vesicles include the immunogens Naph (Neisserial surface protein A, ADL16114), 287 protein (ADL16113) and 741 protein (ADL16112); and the use of outer membrane vesicle compositions as a medicament, especially for raising an immune response in a patient. The method is useful for manufacturing an outer membrane vesicle preparation as a vaccine against Neisseria meningitidis serogroup B. The present sequence represents Neisseria meningitidis serogroup B. The present sequence
                                                                                                                                                                                                                 Producing an outer membrane vesicle (OMV) preparation from a bacterium, useful as a vaccine against Neisseria meningitidis serogroup B, comprises disrupting the bacterial membrane in the absence of deoxycholate
                                                                                                                                                                                                                                                                                                                                                Disclosure, Fig 3; 20pp; English.
                                                                                                                       Rappuoli
                       30-AUG-2002; 2002GB-00020194.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             New receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumor associated antigens, useful treating a neoplastic disease or tumor, and infectious diseases.
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100.0%; Pred. No. 1.1e-86;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                      99US-0173371P.
                                                                                                                                                                     28-DEC-2000; 2000US-00751708
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Matches 174; Conservative
                       Neisseria meningitidis.
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                                                                   US2003157113-A1
                                                                                                                                                                                                                                                                     (TERM/) TERMAN
                                                                                                                                                                                                                      28-DEC-1999;
                                                                                                                    21-AUG-2003
                                                                                                                                                                                                                                                                                                                           Terman DS;
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                                                                                                                                                   PAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
                                                                                                 1 MKKALATLIALALDAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                         PAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
                                                                         1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                      Gaps
                                                                                                                                                                                                                                               SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisserial surface protein A; NspA; refolding; recombinant produc vaccine; subunit vaccine; prevention; diagnosis; meningococcus; invasive bacterial disease; bacteraemia; meningitis; Neisseria gonorihoeae; gonorrhoea; mature protein; strain H44/76;
                                                                                                                                                                                                                           SQTSIGLGULTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF
                                      ö
   Length 174;
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis H44/76 full-length NspA protein.
100.0%; Score 868; DB 8;
100.0%; Pred. No. 1.1e-86;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                              ADL13428 standard; protein; 174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis; H44/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   ADL13428;
                                                                                                                                                                                                                                                                                                                                          RESULT 5
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Outer membrane vesicle preparation; OMV; detergent-free; physical disruption; vaccine; serogroup B; NspA; Neisserial surface protein A; immunogen.

Neisseria meningitidis

HO2004019977-A2

11-MAR-2004.

01-SEP-2003; 2003WO-IB004293.

Neisseria meningitidis NspA for use in vaccine.

(first entry)

03-JUN-2004

SXXXXXXXXXXXXXXX

ADL16114;

ADL16114 standard; protein; 174 AA

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The invention relates to an isolated refolded Neisserial surface protein to a (NspA) from Neisseria meningitidis or Neisseria gonorthoeae. The invention also relates to the method of refolding an NspA protein; an alkaline refolding buffer comprising ethanolamine and SB-12 (3-dimethyldodecylammoniopropanesulphorate) for refolding an NspA protein; a dimethyldodecylammoniopropanesulphorate) for refolding an NspA protein; a pharmaccutical composition comprising the refolded NspA protein; a carrier and optionally one or more other Neisserial antigens; a method of preventing or treating a Neisserial infection; an antibody immunospecific for the NspA protein; and diagnosing a Neisserial infection. NspA has conseed by Neisseria meningitidis (meningococcus), which causes invasive for the development of subunit vaccines for the treatment of infections caused by Neisserial diseases such as bacteraemia and meningitia, or Neisserial conseases such as bacteraemia and meningitis, or Neisserial conseases used in the development of gonorrhoea. Recombinantly produced consequently unable to adopt thair bologically active conformations, and frequently unable to adopt thair bologically active conformations, and frequently unable to adopt thair bologically active conformations, and yields may be very low due to mis-folding and aggregation of the protein. The method of the invention provides an improved method for refolding the conformation and it is possible to increase the recovery of active protein form partly purified inclusion bodies in amounts up to 100% the invention provides an improved Neph protein is useful for preparing a composition for diagnosing, treating or preventing infection caused by Neisseria meningitidis or Neisseria gonorrhoeae. The maximinities of the invention for diagnosing, treating or preventing the medical propers of the full-length NspA protein form partly prificed may be very buffered medical for preparing a composition for diagnosing, treating or preventing and aggrees described or preparation of the fu
                                                                                                                                   /note= "The corresponding residue in the mature protein shown in Fig 2 (residue 149) is Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New refolded NapA protein, useful for preparing a composition for diagnosing, treating or preventing infection caused by Neisseria meningitidis or Neisseria gonorrheae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Poolman J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goraj K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feron C,
                                                                                                                                                                                                                                                                                                                                                                                      GLAXOSMITHKLINB BIOLOGICALS SA. RIJKSUNIV UTRECHT.
                       l. .19
/label= Signal_peptide
Location/Qualifiers
                                                                                        'label= Mature_NspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 3; 62pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Denoel P,
                                                                                                                                                                                                                                                                                                  28-AUG-2003; 2003WO-EP010085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tommassen J, Weynants V;
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meningitidis H44/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADL13427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 174 AA;
                                                                                                                Misc-difference
                                                                                                                                                                                                          WO2004020452-A2
                                                                                                                                                                                                                                                     11-MAR-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biemans
                                                                                                                                                                                                                                                                                                                                                                                           (GLAX )
                     Peptide
                                                                  Protein
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Sequence 174 AA; 19 121 121 셤 셤 ጵ ò δ ö 9 9 1 MKKALATLIALAPAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR Gaps ö Length 174; Indels 100.0%; Score 868; DB 8; 100.0%; Pred. No. 1.1e-86; ive 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 174; Conservative 61 61

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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition comprising liposome associated with isolated polypeptide or polynucleotide derived from Neisseria meningitidis strain 608B, or its fragment or analog, useful for inducing an immune response against N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKKALATLIALALPAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
174
                   121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKP
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 868; DB 8; Best Local Similarity 100.0%; Pred. No. 1.1e-86; Matches 174; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                NspA; vaccine; antibacterial; meningitis.
                                                                                                                                                                                                                             N meningitidis strain 608B NspA protein.
                                                                                                                         ADL24352 standard; protein; 174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          30-AUG-2002; 2002US-0406980P.
                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-2003; 2003WO-CA001452.
                                                                                                                                                                                            03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SHIR-) SHIRE BIOCHEM INC
                                                                                                                                                                                                                                                                                                    Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-239123/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martin D, Rioux S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADL24351.
                                                                                                                                                                                                                                                                                                                                     WO2004019976-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      meningitidis.
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                                                                                                                                                            ADL24352;
 121
                                                                                       RESULT 6
ADL24352
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The invention relates to a composition for treating a tumor or neoplastic disease in a subject. Also described: (1) a mammalian cell comprising an exogenous nucleic acid encoding a superantigen expressed in the cell, which cell also produces or expresses all alpha-anomers of monoglycosylceramide or diglycosylceramide; where expression of the manne or diglycosylceramide is capable of eliciting an antitumor immune response in a mammal into which the cell is introduced; (2) treating a tumor or neoplastic disease in a subject; (3) preparing a population of immunotherapeutic T or natural killer T (NKT) cells useful to treat a tumor or neoplastic disease in a subject; (4) an apoptotic cell preparation of limmunotherapeutic preparating a tumor or local susfic disease in a subject, comprising a cell population that has been transfected with the above apoptotic preparation or lysate, thus, condering the cell effective in presenting material expressed from transfecting nucleic acid or material ingested to the immune system of a mammal to elicit an anti-tumor immune response. The composition and methods are useful for treating tumores or neoplastic diseases The consent sequence represente a Neisseria meningitidis protein sequence which induces meningococcal meningitis, which is given in the exemplification of the present invention. Note - The sequence data for this patent is not represented in the printed specification, but was considered to be taken for the contract of this patent is electrically from the USPTO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition for treating a tumor or neoplastic disease in a subject comprises conjugates comprising superantigen polypeptides or nucleic acids with other molecules that produce a tumoricidal response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                   tumor; neoplasm; gene therapy; immunotherapy; cytostatic; meningitis.
                                                                                                                                              Neisseria meningitidis meningococcal meningitis protein SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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100.0%; Pred. No. 1.1e-86;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 36; 125pp; English.
                 AEA03010 standard; protein; 174 AA.
                                                                                                                                                                                                                                                                                                                                                        08-SEP-2004; 2004US-00937758
                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-2000; 2000US-00650884
                                                                                                   (first entry)
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Best Local Similarity 100.
Matches 174; Conservative
                                                                                                                                                                                                                            Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2005-394926/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (TERM/) TERMAN D S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AEA03009
                                                                                                                                                                                                                                                                      US2005112141-A1.
                                                                                                                                                                                                                                                                                                               26-MAY-2005.
                                                                                                     28-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Terman DS;
                                                            AEA03010;
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AEA03010
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The invention relates to a novel composition comprising outer-membrane vesicles (OWV) prepared from a first strain of Neisseria meningitidis and 1 or more proteins which are present in OWVs prepared from a second strain of N. meningitidis, but which are not present in OWVs prepared from the first strain. The composition of the invention demonstrates antibacterial and antiinflammatory activities and may be useful in the field of meningococcal biochemistry, in particular the trafficking and localisation of meningococcal infections, possibly via the prevention or treatment of meningococcal infections, possibly via the production of a vaccine or gene therapy. The current sequence is that of a Neisseria meningitidis MCSB outer-membrane vesicle (OWV)-related membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New compositions having outer-membrane vesicles and proteins from Neisseria meningitidis, useful in the field of meningococcal biochemistry, in particular for preventing and/or treating meningococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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                                                                                                                                                                                                                                              Neisseria meningitidis MC58 OMV-related membrane protein - SEQ ID 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                 outer-membrane vesicle, antibacterial; antiinflammatory;
meningococcal protein trafficking; localisation; infection; vaccine;
                 121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKNNTVKNVRSGBLSVGVRVKF 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; SEQ ID NO 69; 79pp; English.
                                                                                                                                 ADP08236 standard; protein; 174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-2003; 2003WO-IB006281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-NOV-2002; 2002GB-00026734
27-MAR-2003; 2003GB-00007131
                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis MC58
                                                                                                                                                                                                        26-AUG-2004 (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     W02004046127-A2
                                                                                                                                                                                                                                                                                                                             gene therapy.
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Sequence 174 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for identifying and quantifying one or more proteins in complex mixtures by selectively isolating peptides not containing the relative concentration of one or more proteins and determining the relative concentration of one or more proteins in different samples from the ratio between the areas of estimated different samples from the ratio between the areas of estimated to ach sample or samples of proteins; (b) chemically or chemically different sample or samples of proteins; (b) chemically modifying in each sample or samples (a) peptides obtained in step (a); (c) isolating the NHW peptides by cation exchange chromatography from the mixture of peptides obtained in step (b); (d) idontifying proteins by mass spectrometry analysis of the NHW peptides obtained in step (c); (e) differential isotopic labeling of protein samples previously to step (a) or during steps (a) or (b) and immediately mixing at least a portion of the samples; and (f) relative quantifying of mixing at least a portion of the samples; and (f) relative quantifying of identified in step (d), as well as from the ratio between the areas of identified in step (d), as well as from the ratio between the areas of centimated theoretical spectra of the pair of NHM peptides, generated in step (d). Also described is a kit for the identification and quantification of proteins in complex mixtures, which comprises the method and entioned above. The method and kit are useful for identifying or quantifying proteins, such as those with vaccinal, therapeutic or capanets a surface protein A, which is used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying and quantifying proteins in complex mixtures by selectively isolating peptides not containing histidine nor arginine from each protein, and determining the relative concentration of proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lopez LJG;
   121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perez VAB, Valdes JG,
                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis group B surface protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      protein quantitation; surface protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; SEQ ID NO 20; 91pp; English.
                                                                                                                                                                    AEB93444 standard; protein; 174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dorta-Duque JFD,
Peyt RP, Gil FMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-NOV-2004; 2004US-00988943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-NOV-2003; 2003CU-00000269
                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DORTA-DUQUE J F D
PEREZ V A B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VALDES J.G.
LOPEZ L.J.G.
PALOMARES G.R.P.
FEYT R.P.
GIL F.M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feyt RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BETANCOURT N L H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-596348/61.
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different samples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-AUG-2005.
                                                                                                                                                                                                                                                                                                   20-0CT-2005
                                                                                                                                                                                                                                      AEB93444;
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(FEYT/)
(GILF/)
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(LOPE/)
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                                                                                                                                  AEB93444
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invention

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                                                                                                                                      PAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                          61 PAVDYTRYKNYKAPSTDPKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition comprising liposome associated with isolated polypeptide or polynuclectide derived from Neisseria meningitidis strain 608B, or its fragment or analog, useful for inducing an immune response against N. meningitidis.
                                                                     1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                  1 MKKALATLIALALPAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                  Gaps
                                                                                                                                                                                                                               121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                           SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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 Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "wild-type Gly substituted by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "wild-type Asp substituted by Asn"
                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutein; mutant; NspA; vaccine; antibacterial; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                          N meningitidis strain 608B modified NspA protein #1
Score 864; DB 9;
Pred. No. 2.9e-86;
                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    ADL24383 standard; protein; 174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-AUG-2002; 2002US-0406980P.
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-239123/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martin D, Rioux S;
              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004019976-A2
                                                                                                                                                                                                                                                                                                                                                                                                         03-JUN-2004
                Best Local Sim
Matches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAR-200
                                                                                                                                                                                                                                                                                                                                                                      ADL24383;
                                                                                                                                        61
                                                                                                                                                                                                             121
Query Match
                                                                                                                                                                                                                                                                                                     RESULT 10
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Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IAFB-) IAF BIO VAC INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-443187/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT39042.
                      Sequence 174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAR-1995;
04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9629412-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-1996;
                                                                                                                                                                                                                                                                                               16-OCT-2003
22-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-SEP-1996
                                                                                                                                                                                                                                                                           AAW04894;
                                                                                                                                 61
                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                             AAW04894
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                                                                                                                                 120
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                                                                                                                                            PAVDYTRYKONYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLAGSNSF
                                                                                      1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSIGSAKGFSPRISAGYRINDLR
                                                                                                                                 PAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
                                                                                                                                                                                                                                                                                                                                                   Proteinase K reistant, Neisseria meningitidis; Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
                                                                Gaps
                                                                                                                                                                                      SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGRLSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against,
diagnosis of, N. meningitidis infection.
                                                                                                                                                                           SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGBLSVGVRVKF 174
                                                                .;
0
                                                                                                                                                                                                                                                                                                                                Proteinase K resistant N. meningitidis 22 kD surface protein.
                                             Length 174;
                                           Score 857; DB 8; Length 17
Pred. No. 1.7e-85;
1; Mismatches 1; Indels
 and the wild-type NapA protein shown in Figure 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rioux C;
                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis; strain 24063
                                                                                                                                                                                                                                                                                                                                                                                                                                         20. 174
/label= mat protein
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     1. .19
/label= sig_peptide
                                                                                                                                                                                                                                                      AAW04893 standard; protein; 174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hamel J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Fig 9; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-CA000157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-00406362.
                                          Match 98.7%;
Local Similarity 98.9%;
ues 172; Conservative
                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IAFB-) IAF BIO VAC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martin D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-443187/44.
N-PSDB; AAT39041.
                      Sequence 174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9629412-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAR-1995;
04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brodeur BR,
                                                                                                                                                                                                                                                                                               16-OCT-2003
22-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-SEP-1996.
                                                                                                                                                                                                                                                                           AAW04893;
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                                                                                                                                                                            121
                                                                                                                                                                                                121
                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                Matches
                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                             AAW04893
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                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                           61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                                                                                                                                                                                       1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                      1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteinase K reistant; Neisseria meningitidis; Neisseria gonorrhoeae;
antibody; detection; probe; surface protein.
                                                                                                                                                                                                                                                                                                                                                                                                 SOTSTGLGVLAGVSYAVTPNVDLDAGVRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against,
diagnosis of, N. meningitidis infection.
                                                                                                                                                                                                                                                                                                                                                                  SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteinase K resistant N. meningitidis 22 kD surface protein.
      Length 174
                                                                 3; Indels
Score 854; DB 2;
Pred. No. 3.7e-85;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hamel J, Rioux C;
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/label= mat_protein
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/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW04894 standard; protein; 174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis; strain b2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Fig 10; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00406362.
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      98.4%;
98.3%;
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(first entry)
Query Match
Best Local Similarity 98.3
Matches 171; Conservative
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1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a new gram-negative bacterial bleb presenting on its surface the PorB outer membrane protein from Chlamydia trachomatis, or a protective antigen from C. pneumoniae. The invention is useful for preventing C. trachomatis or C. pneumoniae infection in a host. The present amino acid sequence represents a Neisseria gonorrhoeae protein as described in the invention
                                                                                                                      FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outer
from
                                                                                            1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                               1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                     Gaps
Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                            Novel gram-negative bacterial bleb presenting on its surface PorB membrane protein from Chlamydia trachomatis or protective antigen Chlamydia pneumoniae, useful for preventing Chlamydia infection.
                                                                                                                                                                                                                                                                                                              Gram-negative bacterial bleb; PorB; outer membrane protein;
Chlamydia trachomatis infection; Chlamydia pneumoniae infection;
protective antigen; antibacterial; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 174;
                                       Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 825; DB 5; Length 17 ilarity 94.3%; Pred. No. 5.6e-82; Conservative 2; Mismatches 8; Indels
                                                           8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poolman J, Verlant VGCL;
                                      Score 825; DB 2;
Pred. No. 5.6e-82;
2; Mismatches 8
                                                                                                                                                                                                                                                                                             Neisseria gonorrhoeae outer membrane protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                  ABG91063 standard; protein; 174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 54; 75pp; English
                                      95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                  08-FEB-2002; 2002WO-EP001356
                                                                                                                                                                                                                                                                                                                                                                                                                                      08-FEB-2001; 2001GB-00003169
                                                                                                                                                                                                                                                                         (first entry)
                                                           Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lobet Y,
                                                                                                                                                                                                                                                                                                                                                      Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-657510/70.
                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABS67381.
                    Sequence 174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 174 AA;
                                                                                                                                                                                                                                                                                                                                                                           WO200262380-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Simil
Matches 164;
                                                                                                                                                                                                                                                                         29-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berthet FJ,
                                                                                                                                                                                                                                                                                                                                                                                              15-AUG-2002
                                                                                                                      61
                                                                                                                                                                                                                                                      ABG91063
                                        Query Match
                                                   Best Local
                                                                                                                                                                                                              RESULT 13
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PAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteinase K reistant; Neisseria meningitidis; Neisseria gonorrhoeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against,
diagnosis of, N. meningitidis infection.
                                                                                                                                       174
                                                                                         SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                        Proteinase K resistant N. meningitidis 22 kD surface protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody; detection; probe; surface protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hamel J, Rioux C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis; strain MCH88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .19
/label=_sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                             ż
                                                                                                                                                                                                                                                           AAW04892 standard; protein; 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Fig 8; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-CA000157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00406362.
                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IAFB-) IAF BIO VAC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martin D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-443187/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT39040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 175 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                    16-OCT-2003
22-DEC-1996
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  61
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Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                               RESULT 14
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Gaps

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1 WKKALATLIALALPAPATAEGASGFYVQADAAHAKASSLGSAKGFSPRISAGYRINDLR 60

Similarity

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The present invention relates to a pharmaceutical composition comprising a liposome associated with an isolated polypeptide derived from Neisseria meningitidis strain 608B, where the polypeptide is the NBA protein. The composition is useful for inducting an immune response against N. meningitidis, for preventing and/or treating N. meningitidis infection and for treating and/or preventing neisserial infection chosen from N. meningitidis, N. gonorrhoeae, N. lactamica and N. polysaccharea. It is useful for treatment or prophylaxis of meningitis and meningoccaemia, in a host. The host is a mammal, preferably a human and more preferably an adult human. The present sequence is a modified version of the Neisseria meningitidis strain 608B NBpA protein. Note: This sequence is not shown in the specification but has been created based on the information given
1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSFRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition comprising liposome associated with isolated polypeptide or polynucleotide derived from Neisseria meningitidis strain 608B, or its fragment or analog, useful for inducing an immune response against N.
                                                  PAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS
                                                                                                                       121 PSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                     PSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGBLSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35. .36
/note= "wild-type NspA residues 36-43 deleted"
                                                                                                                                                                                                                                                                                                                                                                mutein; mutant; NspA; vaccine; antibacterial; meningitis.
                                                                                                                                                                                                                                                                                                                              meningitidis strain 608B modified NspA protein #3
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers Misc-difference 35. .36
                                                                                                                                                                                                                          ADL24385 standard; protein; 166 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Page; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-2002; 2002US-0406980P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-2003; 2003WO-CA001452
                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SHIR-) SHIRE BIOCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-239123/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martin D, Rioux S;
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                                                                                                                                                                                                                                                                                           03-JUN-2004
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1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR

Query Match
94.5%; Score 820; DB 8; Length 166;
Best Local Similarity 95.4%; Pred. No. 1.8e-81;
Matches 166; Conservative 0; Mismatches 0; Indels

and the wild-type NspA protein shown in Figure 1.

Sequence 166 AA;

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FAVDYTRYKMYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                       53 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 112
1 MKKALATLIALALPAAALAEGASGFYVQADAAHAK-----KGFSPRISAGYRINDLR 52
                                                                                                                                                                 113 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVRNVRSGELSVGVRVKF 166
                                                                                                                                         121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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completed: January 11, 2006, 15:18:36 he : 79 secs Search comp Job time : THIS PAGE BLANK (USE 10)

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GenCore version 5.1.6 (c) 1993 - 2006 Compugen Ltd.
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- protein search, using sw model OM protein January 11, 2006, 15:15:42; Search time 40 Seconds (without alignments) 418.543 Million cell updates/sec Run on:

US-10-650-123-2

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 200000000 Maximum

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR Database

\*:08

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	outer membrane pro	outer membrane pro	protein	protein-		protein			protein	protein	protein	protein	protein	protein															
SUMMARIES	. QI	G81174	B81932	S16610	S16611	S16613	S16612	KONHO	836343	S16614	S16616	S08514	\$20043	S04380	KONH2C	S72343	836329	S16617	S36342	S36341	836350	KONH8	S36348	836349	S16619	S36346	PL0038	v	F64124	∞ .
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	* Query Match Length	174	174	261	260	338	258	260	237	257	266	258	254	270	268	283	234	282	234	234	233	234	234	238	261	243	248	238	178	239
•	Query Match	99.5	98.4		27.9			27.8	27.7	27.7	27.5	27.4	27.3	27.3		27.2		26.8										25.2		
	Score	864	854	244.5	242	241.5	241	241	240.5	240.5	239	238	237	237	236.5	236	232.5	232.5	232	232	231	226	226	226	226	224.5	221	219	217	215
	Result No.	-	7	9	4	2	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

opacity protein op	opacity protein op	opacity protein op	opacity protein ho	opacity protein op	opacity protein op	opacity protein-re	opacity protein-re	probable outer mem	outer surface prot	hypothetical prote	probable outer mem	opacity protein op	opacity protein op	heat resistant agg	heat resistant agg
S28627	S44706	S44707	I64187	S77737	S20044	808513	T10256	AH0541	AH3012	G98271	F64066	S16286	S44712	AG3556	I54668
N	7	~	7	7	~	~	0	7	7	~	~	0	0	~	N
247	214	235	121	210	187	168	170	239	281	284	70	201	192	284	264
23.7	23.4	21.8	20.7	17.3	16.2	15.6	15.6	15.2	14.9	14.9	14.6	14.6	14.5	14.1	14.0
	'n	9.5	180	50.5	141	135	135	132	29.5	29.5	26.5	26.5	126	122	21.5
205.5	203	18		ä					_	_	_	_			Н

## ALIGNMENTS

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outer membrane protein NegA NWB0663 [imported] - Neisseria meningitidis (strain MC58 ser C; Species: Neisseria meningitidis (Species: Neisseria meningitidis (Species: Neisseria meningitidis (Species: Neisseria) (Species

A;AUThors: Grandl, G., Sur, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Itle: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755; PMID:10710307

A;Accession: G81174
A;Status: preliminary
A;Molecule type: DMA
A;Reaidues: 1-174 <TET>
A;Coss-references: UNIPROT:QSRP17; UNIPARC:UPI00000D41C1; GB:AE002420; GB:AE002098; NID
A;Cross-references: UNIPROT:QSRP17; UNIPARC:UPI0000D41C1; GB:AE002420; GB:AE002098; NID
C;Genetics:
A;Gene: NMB0663

ö 99.5%; Score 864; DB 2; Length 174; 99.4%; Pred. No. 6.9e-70; vative 0; Mismatches 1; Indels Best Local Similarity 99.4 Matches 173, Conservative Query Match

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9 9 1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 1 MKKALATLIALALPAAALAEGASGPYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 셤 ઠે

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61 FAUDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120 셤

121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVROVRSGELSAGVRVKF 174 121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174 g ઠ

# RESULT 2

outer membrane protein NWA0862 [imported] - Neisseria meningitidis (strain 22491 serogro C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004 C;Accession: B819132 R;Pathill, J; Achtman, M; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel FGIXONA, S., Jagelg, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2040 A,Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A,Reference number: AB1775; MUID:2022556; PMID:10761919
A,Accession: B81932
A,Status: preliminary

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Score 242; DB 2; Length 260; Pred. No. 3.2e-14;
                        SAGYRINDLRFAVDYTRYKNY-
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                                                                                                                                                                                                                                                                                                                                   RVKF 174
                                                                                                                                                                                                                                                                                                                                                                                   258 RYRF 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S16611
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C.Species neisseria gonorrhoeae (strain MS11) (fragments)
NiAlternate names outer membrane protein opaK
C.Species Neisseria gonorrhoeae
A.Warlety: strain MS11
C.Species 13.-dan-1955 Heaquence_revision 17-oct-1997 #text_change 17-oct-1997
C.Accession. Sifetio
R.Shant, K.S.; dibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, P.; Stern, A.; Kupsch, Mol. Mcrobiol. S. 18610, MUD:9211476; PMD:1815562
A.Fitte: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fami
A.Reference number: Sifetio, MUD:9211476; PMD:1815562
A.Fitte: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fami
A.Reference number: Sifetio, MUD:9211476; PMD:1815562
A.Fitte: The opacity proteins of Neisseria gonorrhoeae strain MS11, variant 4.8
A.Focasion. Sifetio
A.Focasion. Sifetion. Sifetion
A.Focasion. Sifetion. Sifetion. Sifetion
C.Genetics
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C.Genetics
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             A,Residues: 1-174 <PAR>
A,Cross-references: UNIPROT:P95372; UNIPARC:UPI0000D41C0; GB:AL162754; GB:AL157959; NID
A,Experimental source: serogroup A, strain 22491
C,Genetics:
A,Gene: nspA; NMA0862
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                                                                                                                                                                                                                                                                                                                                                                                                                FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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21 AQAASEGNGRĞPYVQADLAYAAERITHDYPEPTGAKKGTTISTVSDYFRNIRTHSIHPRV 80
                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                             1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSIGSAKGFSPRISAGYRINDLR
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                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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                                                                                                                                                                           Length 174;
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                                                                                                                                                                                                                                3; Indels
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                                                                                                                                                                           98.4%; Score 854; DB 2;
98.3%; Pred. No. 5.4e-69;
ive 0; Mismatches 3.
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Pred. No. 1.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.2%;
29.9%;
                                                                                                                                                                        Query Match
Best Local Similarity 98.3
Matches 171; Conservative
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A;Molecule type: DNA
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opacity protein opad precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
Nylternate names: outer membrane protein opa58
C;Species: Neisseria gonorrhoeae
A;Variety: strain MS11
C;Date: 04-Jun-1997 #sequence revision 17-Oct-1997 #text_change 09-Jul-2004
C;Accession: S16611; S36345; S28624
C;Accession: S16611; S36345; S28624
Mol. Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 24-260 <KUP>
A;Cross-references: UNIPARC:UP10000130D60; EMBL:Z18937; NID:g49333; PIDN:CAA79370.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms di
A;Reference number: S36328; MUID:93178439; PMID:8440254
A;Accession: S36345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       number of translated repeat e
the protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-260 <-BHA.
A; Cross-references: UNIPROT: Q04882; UNIPARC: UPI00001781FB; EMBL: X52371
A; Experimental source: strain M311, variant 4.8
A; Note: the authors did not translate the sequence for the signal peptide
A; Note: expression of opacity proteins is regulated by the number of translated b; repeats place the start codon in frame with the rest of the protein
R; Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
EMBO J. 12, 641-650, 1993
                                                                                  81 SVGYDFGGWRIAADYARYRKWNNNKYSVSIKELLRNKGNGNRTDLKAENQENGTFHAVSS 140
                                                                                                                                                                              116
                                                                                                                                                                                                                                     ----SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGV 170
                                                                                                                                                                                                                                                                                                                                                                                                     201 QNAHRESDSIRR--VGLGAVAGVGIDITPNLTLDAGYRYHYWGRLENTR-PKTHEASLGV 257
82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isuperfamily: opacity protein
;Keywords: cell surface component; transmembrane protein
;1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
;24-260/Product: opacity protein opal #status predicted <MAT>
;34-42/Domain: transmembrane #status predicted <TMI>
;43-74/Domain: extracellular #status predicted <EXII>
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A;Note: expression of opacity proteins is regulated by the
of repeats place the start codon in frame with the rest of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;95-133/Domain: extracellular #status predicted <EXT2>F;101-128/Region: hypervariable region HV1
F;134-148/Domain: transmembrane #status predicted <TM4>F;154-144/Domain: transmembrane #status predicted <TM5>F;155-211/Domain: extracellular #status predicted <TM5>F;170-211/Region: hypervariable region HV2
F;212-224/Domain: transmembrane #status predicted <TM6>F;212-224/Domain: transmembrane #status predicted <TM6>F;212-224/Domain: transmembrane
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;75-83/Domain: transmembrane #status predicted <TM2>
;88-94/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                              IGASAIYDFDTQSPVKPYLGARLSLN--RASVD
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KKPSLLPSSLGSARGES-4AGFYVQADAAHAKASSSLGSARGES-47   KKPSLLPSSLLPSSAAQAAGEDHGGPYVQADLAYAYEHITHDYPEQTDPSKAKISTVSD 65   KKPSLLPSSLLPSSAAQAAGEDHGGPYVQADLAYAYEHITHDYPEQTDPSKAKISTVSD 65   KKPSLLPSSLAYSTRADLARYKWYAYAY	Db 157 HERNSVOYDEGGRIAADYEKTRANDIKTSVOIKELENKRODKKTENGENGTFHAD 216  Oy 81 YSIGASAIYDPDTGGSVERIAADYEKTRANDIKTSVOIKELENKRODKKTENGENGTFHAD 216
rne protein  redicted <sig> MAT&gt;  th 338;  ls 79; Gaps 9;  SLGSAKGF 46                                       </sig>	Figa-44/Domain: transmembrane #status predicted (*MI) Figa-44/Domain: extracellular #status predicted (*MI) Figa-44/Domain: extracellular #status predicted (*MI) Figa-94/Domain: transmembrane #status predicted (*MI) Figa-14/Domain: transmembrane #status predicted (*MI) Figa-12/Fkegion: hypervariable region HV2 Figa-21/Domain: transmembrane #status predicted (*MI) Figa-21/Domain: transmembrane #status predicted (*MI) Figa-21/Domain: transmembrane #status predicted (*MI) Figa-22/Domain: transmembrane #status predicted (*MI) Figa-22/Domain: transmembrane #status predicted (*MI) Figa-22/Domain: transmembrane #status predicted (*MI) Figa-23/Domain: transmembrane #status predicted (*MI) Figa-24/Domain: transmembrane #status predicted (*MI) Figa-24/Domain: transmembrane #status predicted (*MI) Figa-21/Fkegion: hypervariable factus hypervariable factu

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A;Title: "Variable opacity (Opa) outer membrane proteins account for the cell tropisms di A;Reference number: S36328; MUID:93178439; PMID:8440254 A;Accession: S36343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 HSIHPRVSVGYDFGGWRIAADYARYRKWSDNKYSVSIKNMRVHKHNSNRKNLKTENQENG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --PKLYSIGASAIYDPDTQSPVKPYLGARLSLN--RASVD-------LGG- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                  73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       opacity protein opa57 - Neisseria gonorrhoeae (strain MS11) (fragment)
N;Alternate names: outer membrane protein opa57
C;Species: Neisseria gonorrhoeae
A;Variety: strain MS11
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S36343; S28626
R;Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
EMBO J. 12, 641-650, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------KNYKAPSTD--
                                                                                                                                                                                                                                                                                                                                                                    6 ATLIALALPAAALAEGASGFYVQADAAHA------KASSSLGSAKGFS-----
                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                   84;
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                                                                                                                                                                                                 DB 1; Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <MAT>
                                                                                                                                                                                                                                                                                       64; Indels
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A;Note: expression of opacity proteins is regulated by the
of repeats place the start codon in frame with the rest of
                                                                             <EXT4>
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                                  F;228-236/Domain: transmembrane #status predicted <TM7>
F;237-251/Domain: extracellular #status predicted <EXT4
F;252-260/Domain: transmembrane #status predicted <TM8>
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F;229-237/Domain: transmembrane #status predicted <TM8>
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                                                                                                                                                                                                     ; Score 241; DB 1; Pred. No. 4e-14; 30; Mismatches
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#status
                                                                                                                                                                                                     27.8%;
                                                                                                                                                          Query Match
Best Local Similarity 25....
Best Local Similarity 25....
72; Conservative
F;212-224/Domain: transmembrane
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Best Local Similarity 29.69
Matches 71; Conservative
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EASLGVRYRF 260
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A; Residues: 25-260 < MEX>
A; Conclue type: DNA
A; Residues: 25-260 < MEX>
A; Cross-creferences: UNIPARC:UP10000130D59; EMBL:Z18927; NID:g49323; PIDN:CAA79360.1; PID
C; Genetics:
C; Genetics:
A; Gene: opac
C; Superfamily: opacity protein
C; Keywords: cell surface component; transmembrane protein
C; Keywords: cell surface component; transmembrane predicted < MID:
C; Reymonds: cell surface component; predicted < MID:
F; 25-260/Product: opacity protein opac #status predicted < MAT>
F; 25-260/Product: opacity protein opac #status predicted < MAT>
F; 25-41/Domain: transmembrane #status predicted < TMD>
F; 25-61/Region: benivariable region HV2
F; 102-129/Region: hypervariable region HV2
F; 102-129/Region: transmembrane #status predicted < TMS>
F; 102-129/Region: hypervariable region HV2
F; 112-11/Region: hypervariable region HV2
F; 112-11/Region: hypervariable region HV2
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A; A; Residues: 1-260 < SHRA
A; A; Residues: 1-260 < SHRA
A; A; Cross-references: UNIPROT: P11296; UNIPARC: UPI00001747E3; EMBL: X52370
A; Experimental Bource: strain MS11, variant 4.8
A; Whote: the authors translated the codon CCA for residue 32 as Thr
A; Note: the authors translated the sequence for the signal peptide
A; Note: the authors did not translated the sequence for the signal peptide
A; Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
R; Stern, A: Brown, M.; Nickel, P.; Meyer, T.F.
Cell 47, 61-71, 1986
A; Ritle: Opacity genes in Neisseria gonorrhoeae: control of phase and antigenic variatic
A; Accession: A24229
A; McBesidues: 25-260 < STRAPA
A; Residues: 25-260 < STRAPA
A; Residues: 25-260 < STRAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                         opacity protein opaC precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

NyAlternate names: opacity protein V0; triosephosphate dehydrogenase

NyAlternate names: opacity protein V0; triosephosphate dehydrogenase

A; Species Neisseria gonorrhoeae

A; Variety: strain MS11

C; Date: 31-Mar-1989 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004

C; Date: 31-Mar-1989 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004

C; Date: 31-Mar-1989 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004

R; Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, Mol. Microbiol. S, 1889-1901, 1991

A; Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a famil A; Reference number: S16610; MUID:92114767; PMID:1815562

A; Molecule type: DNA
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Mostales: 25-260 < XUD>
A;Mostales: 25-260 < XUD>
A;Cross-references: UNIPARC:UPI0000130D59; EMBL:Z18927; NID:g49323; PIDN:CAA79360.1; PIG
R;Meyer, T.P.
submitted to the EMBL Data Library, November 1992
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A;Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms di A;Ritle: AA,Reference number: S36328; MUID:93178439; PMID:8440254
A;Accession: S36328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UP10000130D59
A;Note: this protein is synthesized as a precursor; however, the authors are uncertain
                                               ------SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
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244 R-FKTHEASLGVRYRF 258
                                                                                                                                                                   159 KNVRSGELSVGVRVKF
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    117
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DD 126 NQENGTFHAVSSLGLSAVYDFKLANDKFKPYIGARVAYGHVRHSIDSTKKTTKFLTSSYGG 185  QY 117SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNV 161  DD 186 LANFTVYTEENTQNAHHQSNSIRRVGLGVIAGVGFDITPKLTLDTGYRXHYWGRLENTR-F 244  QY 162 RSGELSVGVRVKF 174  DD 245 KTHEASLGVRYKF 257	Si6616  Si6616  Opacity protein opaD precursor - Neisseria gonorrhoeae (strain MS11) (fragments) C;Species: Neisseria gonorrhoeae A;Variety: strain MS11 C;Bate: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997 C;Accession: S16616 R;Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, P.; Stern, A.; Kupsch, MOL. Microbiol. S, 1889-1901, 1991 A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fami A;Reference number: S16616 A;Rocession: S16616 A;Rocession: S16616 A;Rollocule type: DNA A;Residues: 1-266 < SBHA> A;Residues: 1-266 < SBHA> A;Cros-references: UNIPARC:UPI0000178203; EMBL:X52372	A; Experimental source: strain MSII, variant 4.8 A; Roce: the authors did not translate the sequence for the signal peptide A; Note: the authors did not translate the sequence for the signal peptide A; Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein C; Seperities: opacity protein C; Superfamily: opacity protein C; Superfamily: opacity protein F; 1-10, 11-23/Domain: signal sequence (fragments) #status predicted <sig>F; 24-266/Product: opacity protein opab #status predicted <mat>F; 34-3/Domain: extracellular #status predicted <tmi>F; 37-3/Domain: extracellular #status predicted <tmi>F; 51-60/Region: semivariable region</tmi></tmi></mat></sig>	F;95-83/Domain: transmembrane #status predicted <im2> F;88-94/Domain: transmembrane #status predicted <im3> F;88-94/Domain: transmembrane #status predicted <im3> F;85-139/Domain: extracellular #status predicted <im3> F;101-134/Region: hypervariable region HV1 F;140-154/Domain: transmembrane #status predicted <im4> F;160-170/Domain: transmembrane #status predicted <im5> F;171-217/Domain: transmembrane #status predicted <im5> F;186-233/Region: hypervariable region HV2 F;218-230/Domain: transmembrane #status predicted <im5> F;234-242/Domain: transmembrane #status predicted <im7> F;238-266/Domain: transmembrane #status predicted <im7> F;288-266/Domain: transmembrane #status predicted <im8> Query Match Z7.5\$; Score 239; DB 2; Length 266;</im8></im7></im7></im5></im5></im5></im4></im3></im3></im3></im2>	Best Local Similarity 29.0%; Pred. No. 6.18-14;     Matches 76; Conservative 26; Mismatches 70; Indels 90; Gaps 8;     Qy
17 ALAEGASGFYVQADAAHA	Oy 117SDSFSQTSIGGAUTGVSYAVTPNVDLDAGTRINYIGKVNTYKNYRSGELSVGVRYKF 174	A;Title: The opacity proceins of Neisseria gonorrhoeae strain MS11 are encoded by a family Reference number: S16610; MUID:92114767; PMID:1815562 A;Reference number: S16614 A;Reference number: S16610, MUID:92114767; PMID:1815562 A;Residues: 1-257 < EHAA A;Residues: 1-257	авн нхонно	hypervariable transmembrane transmembrane extracellula: transmembrane transmembrane 27.74 larity 29.28 Conservative LATLIALALPAANI :               SLLFSSILFSSAR

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A;Residues: 1-254 cAHO.
A;Cross-references: UNIPROT:033388; UNIPARC:UPI0000178201; EMBL:X63108
A;Cross-references: UNIPROT:033388; UNIPARC:UPI0000178201; EMBL:X63108
A;Experimental source: strain FAM18; clone pFLOB1700
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
A;Note: only a part of the translation is segulated by the number of translated repeat e of repeats place the start codon in frame with the rest of the protein
opacity protein B precursor (clone prioblino) - Neisseria meningitidis (strain FAMIS)
NiAlternate names: outer membrane protein class 5
Cispecies: Neisseria meningitidis
A;Variety: strain FAMIS
C;Date: 04-Jun-1997 #sequence_revision 04-Jun-1997 #text_change 09-Jul-2004
                                                                                                                                                                                           C;Accession: S20043
R;Aho, B.L.; Dempsey, J.A.; Hobbs, M.M.; Klapper, D.G.; Cannon, J.G.
Mol. Microbiol. 5, 1429-1437, 1991
A;Title: Characterization of the opa (class 5) gene family of Neisseria meningitidis.
A;Reference number: S16286; MUID:92157869; PMID:1787795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 SIGASAIYDFDTQSPVKPYLGARLSLN--RASVDL------GGSD-----
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C;Keywords: cell surface component; transmembrane protein
C;Keywords: cell surface component; transmembrane predicted <SIG>
F;1-19/Domain: signal sequence (fragment) #status predicted <KIG>
F;20-254/Product: opacity protein opas #status predicted <MAT>
F;20-254/Product: opacity protein opas #status predicted <MAT>
F;31-39/Domain: transmembrane #status predicted <EXT1>
F;40-69/Domain: extracellular #status predicted <TM2>
F;30-126/Domain: transmembrane #status predicted <TM3>
F;90-121/Rogion: hypervariable region HV1
F;127-141/Domain: transmembrane #status predicted <TM5>
F;127-141/Domain: transmembrane #status predicted <TM5>
F;127-141/Domain: transmembrane #status predicted <TM5>
F;128-205/Domain: transmembrane #status predicted <TM5>
F;128-211/Region: hypervariable region HV2
F;20-218/Domain: transmembrane #status predicted <TM6>
F;212-214/Pomain: transmembrane #status predicted <TM6>
F;213-245/Domain: transmembrane #status predicted <TM6>
F;213-245/Domain: transmembrane #status predicted <TM6>
F;246-254/Domain: transmembrane #status predicted <TM8>
F;246-254/Domain: transmembrane #status predicted <TM8>
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                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: S20043
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A/Ketezenice number: 3008514
A/Molecule type: DNA
A/Residues: 1-58 «STE>
A/CROSS-references: UNIPROT:P10170; UNIPARC:UP1000017820E; EMBL:X06445; NID:944906; PID:
A/CROSS-references: UNIPROT:P10170; UNIPARC:UP1000017820E; EMBL:X06445; NID:944906; PID:
A/CROSS-references: UNIPROT:P10170; UNIPARC:UP1000017820E; EMBL:X06445; NID:944906; PID:
A/Repeats place the strain codon in frame with the rest of the protein
C/Genetics:
A/Gens: Opri
C/Superfamily: opacity protein
C/Superfamily: opacity protein-related protein OPMI #status predicted <AMI.>
C/Superfamily: opacity protein-related protein OPMI #status predicted <AMI.>
C/Superfamily: opacity protein-related predicted <AMI.>
C/Superfamily: opacity opacity predicted <AMI.>
C/Superfamily: opacity protein-related Predicted <AMI.>
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C/Superfamily: opacity protein-related Predicted <AMI.>
C/Superfamily: o
                                                                                                                                                                                                                                                               opacity protein-related protein OPM1 precursor - Neisseria meningitidis (strain C1938) (N'Alternate names: outer membrane protein class 5 (Species: Neisseria maningitidis A,Variety atrain C1938 (C;Species: Neisseria maningitidis C;Species: Neisseria maningitidis C;Species: Neisseria maningitidis C;Species: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004 (C;Accession: S08514 MS. Stern, A.; Meyer, T.P. Mol. Microbiol. 1, S-12, 1987 Mol. Microbiol. 1, S-12, 1987 A;Title: Common mechanism controlling phase and antigenic variation in pathogenic neisse A;Reference number: S08513; MUID: 88260884; PMID: 2455211
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                                                       1:: :: | |:||| :|
246 GRLENTR-FKTHEASLGVRYRF 266
           153 GKVNTVKNVRSGELSVGVRVKP
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GMRYRF 258
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N;Alternate names: outer membrane protein P.IIc
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TR-FKTHEASLGMRYRF 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: protein
A;Residues: 24-34 <BAR>
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Matches 69; Conserv
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Rippalmer, L.; Brooks, G.F.; Falkow, S.

Mol. Microbiol. 3, 663-671, 1999
A.Tille: Expression of gonococcal protein II in Escherichia coli by translational fusion A.Tille: Expression of gonococcal protein II in Escherichia coli by translational fusion A.Trele: Expression of gonococcal protein II in Escherichia coli by translational fusion A.Recession: 804380
A.Recession: 804380
A.Recession: 804380
A.Recession: 804380
A.Recession: 604380; MUID: 89348553; PMID: 2503862
A.Rocession: 804380
A.Rocession: 804380
A.Rocession: 804380
A.Rocession: 804380
A.Rocession: 804380
A.Rocession of opacity protein be required by the number of translated repeat of regate the author of pacity proteins is required by the number of translated repeat of regate place the state codon in frame with the rest of the protein A.Rocession: 816504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 DYFRNIRTHSVHPRVSVGYDFGGWRIAADYARYRKWNNNKYSVSIKELGRNDNSASGVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 KKPSLLPSSLLPSSAAQAAGEGNGRGPYVQADLAYAYEHITHDYPKPTGAKKGTTISTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 GP-----SPRISAGYRINDLRPAVDYTRYK--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KKALATLIALALPAALAEG---ASGFYVQADAAH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.3%; Score 237; DB 2; 27.1%; Pred. No. 9.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72; Conservative
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Best Local Similarity
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KONH2C
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opacity protein P.IIc precursor - Neisseria gonorrhoeae (strain JS3) (fragments)

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C,Accession: 803095; 816360
R, van der Ley, P.
R, van der Ley, P.
A,Title: Three copies of a single protein II-encoding sequence in the genome of Neissers A,Reference number: 803095; MUID:89096501; PMID:3145386
                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-568 «VANA-
A; Residues: 1-568 «VANA-
A; Residues: 1-568 «VANA-
A; Crose-references: UNIPROT: P09888; UNIPARC: UPI0000174784; EMBL: X12625
A; Crose-references: Brrain JG3
A; Note: 241-Val was also found
A; Note: expression of opacity proteins is regulated by the number of translated repeat e
A; Note: expression of opacity proteins is regulated by the protein
B; Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
B; Barritt, D.S.; 2026-2031, 1987
A; Title: Antigenic and structural differences among six proteins II expressed by a singli A; Reference number: $16360; MUID: 87306843; PMID: 3114142
A; Accession: $16360
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A;Variety: strain JS3
C;Date: 31-Mar-1992 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 TDFK-----SVDL----SVDL-----SVDL-----SVDL-----
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F;1-10,1-123/Domain: signal sequence (fragments) #status predicted

F;1-10,1-123/Domain: signal sequence (fragments) #status predicted

F;34-42/Domain: transmembrane #status predicted <TM1>

F;34-42/Domain: extracellular #status predicted <TM1>

F;35-60/Region: semivariable region

F;75-83/Domain: transmembrane #status predicted <TM2>

F;88-94/Domain: transmembrane #status predicted <TM2>

F;95-140/Domain: extracellular #status predicted <TM2>

F;95-140/Domain: extracellular #status predicted <TM2>

F;101-135/Region: hypervariable region HV1
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F;161-171/Domain: transmembrane #status predicted <TM5>
F;172-194/Domain: extracellular #status predicted <EXT3>
F;177-225/Region: hypervariable region HV2
F;220-232/Domain: transmembrane #status predicted <TM6>
F;245-224/Domain: transmembrane #status predicted <TM7>
F;245-255/Domain: extracellular #status predicted <EXT4>
F;260-268/Domain: transmembrane #status predicted <EXT4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: UNIPARC: UPI00001747E5
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SY2343
OpenCity protein opaH precursor - Neisseria gonorrhoeae (isolate 15063G)
NyAlternate names: cell invasion protein opaH
Cispecies Neisseria gonorrhoeae
Cispecies Neisseria gonorrhoeae
A;Variety: isolate 15063G
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: 87243,
M;Haldbeser, LS; Ajioka, R.S; Merz, A.J.; Pusoi, D.; Lin, L.; Thomas, M.; So, M.
A;Haldbeser, LS; Ajioka, R.S; Merz, A.J.; Pusoi, D.; Lin, L.; Thomas, M.; So, M.
A;Accession: 87243,
A;Accession: 87243,
A;Accession: 87243,
A;Accession: 87243,
A;Accession: BNA
A;Roberule type: DNA
A;Roberu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGASAIYDFDTQSPVKPYLGARLSLN--RASVDL------114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 ----GGSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 27.2%; Score 236; DB 2; Length 283
Best Local Similarity 27.9%; Pred. No. 1.2e-13;
Matches 68; Conservative 29; Mismatches 67; Indels
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Job time : 41 secs
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# GenCore version 5.1.6 Copyright (c) 1993 - 2006 Compugen Ltd.

- protein search, using sw model OM protein

January 11, 2006, 15:14:46; Search time 161 Seconds (without alignments) 762.496 Million cell updates/sec Run on:

US-10-650-123-2

1 MKKALATLIALALPAALAE........VNTVKNVRSGELSVGVRVKF 174 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2166443 Total number of hits satisfying chosen parameters: 2166443 segs, 705528306 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	P96943 neisseria m	Q9rp17 neisseria m	neisseria			Q7ar60 neisseria m				neisseria		_	_				O07280 neisseria m			neisseria				Q9k4t4 neisseria l		Q51125 neisseria m	Q9r3p5 neisseria m	neisseria		87	O31176 neisseria m
ID	P96943 NEIME	Q9RP17 NEIME	Q7DDM2_NEIMB	Q9R2R1 NBIME	P95372 NEIME	Q7AR60 NEIMA	Q9RP16 NEIME	Q9RP18 NEIME	P95343 NEIGO	P95371_NEIME		Q65RV6 MANSM	Q65TE2 MANSM	Q51124 NBIMB	Q9CM19_PASMU	Q9R7I9_NEIMB	O07280 NEIME	Q9R718 NEIME	OPAJ_NEIGO	Q9K4T9 NEILA	Q9AE80 NEIME	Q9R9A7_NEIME	OPAK NEIGO	Q9K4T4 NEILA	Q51126 NEIME	Q51125 NEIME	Q9R3P5 NBIMB	OPR1 NEIMC	Q50929 NBIFV	O07287 NEIME	O31176_NEIME
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	Q7BW15 NEIME	O33388 NEIME	Q9K4T3 NEISU	OMPC NEIGO	Q9RQV4 NEIME	Q50943 NEIGO	OPAC NEIGO	007274 NEIME	007925 NEIME	Q51013 NEIGO	007912 NEIME	Q51303 NEISI	Q9K4T5 NEILA	O30753_NRIME	
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	237	237	236.5	236.5	236	236	235	234.5	234	234	233.5	233.5	233	233	
	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

# ALIGNMENTS

MEDLINE=99270944; PubMed=10338491; Plante M., Cadieux N., Rioux C.R., Hamel J., Brodeur B.R., Martin D.; "Antigenic and molecular conservation of the gonococcal NspA F protein."; Infect. Immun. 67;(2855-286) (1999).

De NUCLEOTIDE SEQUENCE.

STRIN=608B;
MEDLINE-99386904; PubMed=10456958;
MEDLINE-99386904; PubMed=10456958;
Caddeux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
Caddeux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
"Bactericidal and cross-protective activities of a monoclonal antibody directed against Neisseria-meningitidis NspA outer membrane protein.";
Infect. Immun. 67(4955-4959(1999).

NUCLECTIDE SEQUENCE.

STRAIN=M986, NG6/88, and NGP165;
Moe G.R., Tan S., Grandf D.M.;
"Differences in Surface Expression of Neisserial Surface Protein A among Weiseeria meningitidis Group B strains.";
Infect. Immun. 0:0-0(1999).
EMBL; W52066; AAC3000.1; -; Genomic\_DNA.
EMBL; AF175680; AAD53283.1; -; Genomic\_DNA.
EMBL; AF175681; AAD53285.1; -; Genomic\_DNA.
EMBL; AF175682; AAD53285.1; -; Genomic\_DNA.
EMBL; AF175683; AAD53286.1; -; Genomic\_DNA.
EMBL; AF175683; AAD53286.1; -; Genomic\_DNA.
EMBL; AF175683; AAD53286.1; -; Genomic\_DNA.
GO; GO:00150280; Eporin activity; IEA.
InterPro; IPR003394; Porin\_opacity.
Pfam; PF02462; Opacity; 1. 

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Name=nspA;
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                                                                                 Length 174;
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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                                      174 AA; 18425 MW; E8B02767DDC6FE19 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moe G.R., Tan S., Granoff D.M.; "Differences in Surface Expression of Neisserial among Neisseria meningitidis Group B strains.";
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(TrEMBLrel. 27, Last sequence update)
                                                                               100.0%; Score 868; DB 2;
100.0%; Pred. No. 8.2e-69;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.5%; Score 864; DB 2; 99.4%; Pred. No. 1.9e-68; ive 0; Mismatches 1;
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EMBL, AF175678; AAD53281.1; -; Genomic_DNA.

PDR; G1174; G81174.

PDB; 1P4T; X-ray; A=20-174.

G0; G0:001620; C:mehxene; IEA.

G0; G0:0015288; F:porin activity; IEA.

InterPro; IPR003394; Porin_opacity.
                       Potential
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01-MAY-2000 (TrEMBLrel. 13, La
01-JUN-2003 (TrEMBLrel. 24, La
Surface protein A.
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QBRP17;
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Q7DDM2;
05-JUL-2004 (TrEMBLrel. 2'
05-JUL-2004 (TrEMBLrel. 2'
                                                                                                    Best Local Similarity 100.
Matches 174; Conservative
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MEDLINES / Sergoroup B; MEDLINES Science. 287.5459.1809; MEDLINES. 20175755; PubMed=10710307; DOI=10.1126/science. 287.5459.1809; Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D., Hickey B.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T.M., Ciecko A., Parkesy D.S., Blair E., Citcon H., Clark B.B., Cotton M.D., Utterback T.R., Khouri H.M., Qin H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKFYLGARLSLARASVDLGGSDSF
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Moe G.R., Tan S., Granoff D.M.;
Moe G.R., Tan S., Granoff D.M.;
"Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningiridis Group B strains.";
Infect. Immun. 0:0-0(1999):
EMBL, ARJ5679; AAD53282.1; -; Genomic_DNA.
EMBL; ARJ75677; AAD53280.1; -; Genomic_DNA.
HSSP; Q9RP17; 1P4T.
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
NCBI_TaxID=487;
                                                                                        Neisseria meningitidis (serogroup B).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales;
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Last sequence update)
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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99.5%; Score 864; DB 2;
Best Local Similarity 99.4%; Pred. No. 1.9e-68;
Matches 173; Conservative 0; Mismatches 1;
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EMBL; AE002099; AAF41081.1; -; Genomic_DNA.
SWR; Q7DDM2; 20-174.
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                              Outer membrane protein NspA.
Name=nspA; OrderedLocusNames=NMB0663;
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GO; GO:0015288; F:porin activity;
InterRro; IFR003394; Porin_opacity
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SROUENCE 174 AR; 18397 MW-
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01-MAY_2000 (TrEMBLrel. 13,
01-FEB-2005 (TrEMBLrel. 29,
Surface protein A.
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Q9R2R1;
                                                                                                                                                         Neisseriaceae; Neisseria.
NCBI_TaxID=491;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                       1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSIGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                          1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVRNVRSGELSAGVRVKF 174
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                              Length 174;
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                                                                                                                                        98.7%; Score 857; DB 2; Length 17.98.3%; Pred. No. 7.8e-68; Wismarches 2; Indels
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98.3%; Pred. No. 1.4e-67;
ive 0; Mismatches 3; Indels
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174 AA; 18355 MW; B8A4AlADA4F6F009 CRC64;
                                                                                       Pfam, PF02462, Opacity, 1. SEQUENCE 174 AA, 18385 MW, ECP6F39A9286910E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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EMBL, U52068; AB841580.1; -; Genomic_DNA. PIR; B81932; B81932.
HSSP; O3RP17; 1P4T.
SMR; P95372; 20-174.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0015288; F:porin activity; IEA.
InterPro; IPR003394; Porin_opacity.
                   GO; GO:0016020; C:membrane; IEA.
GO; GO:0015288; F:porin activity; IEA.
InterPro; IPR003394; Porin_opacity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Outer membrane protein precursor.
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NCBL_TaxID=487;
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Best Local Similarity 98.3
Matches 171; Conservative
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NEDLINE-2022556; PubMed=10761919; DOI=10.1038/35006655;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
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Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
meningitidls 27491-7.
Nature 404:502-506(2009).
EMBS-All62774; CABB4143.1; -; Genomic_DNA.
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"Differences in Surface Expression of Neisserial Surface Protein."
"Differences in Surface Expression of Neisseria meningitidis Group B strains.";
Infect. Immun. 0:0-0(1999).
EMBL; AF175681; AAD53284.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
NCBI_TaxID=487;
                                                                                                                                                                                               Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 AA; 18355 MW; E8A4A1ADA4F6F009 CRC64;
                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                       174 AA
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                                                                                                                                                 Outer membrane protein.
Name=nspA; OrderedLocusNames=NMA0862;
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GO; GO:0015288; F:porin activity; II
InterPro; IPR003394; Porin_opacity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9RP16 NEIME PRELIMINARY;
Q9RP16;
Q7AR60 NEIMA
ID Q7AR60 NEIMA PRELIMINARY;
                                                                                                                                                                                                                                              Neisseriaceae, Neisseria.
NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 98.3
Matches 171; Conservative
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Name=nspA;
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61 PAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99270944; PubMed=10338491; Plante M., Cadieux N., Rioux C.R., Hamel J., Brodeur B.R., Martin D.; Antigenic and molecular conservation of the gonococcal NspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                        Outer membrane protein precursor (Surface protein A).
Nelsseria gonorrhoeae.
Batceria, proteobacteria, Betaproteobacteria, Neisseriales, Neisseriaceae, Neis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mingchun J.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; U52069; AAB41581.1; -; Genomic DNA.
EMBL; AX157539; AAN77898.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential.
1B558EC8A040841A CRC64;
                                                                                                                Last sequence update)
Last annotation update)
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95.0%; Score 825; DB 2;
Best Local Similarity 94.3%; Pred. No. 5.3e-65;
Matches 164; Conservative 2; Mismatches 8
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SMR; P95343; 20-174.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0015288; R:porin activity; IEA.
InterPro; IPR003394; Porin opacity.
                                                                            Created)
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nfect. Immun. 67:2855-2861(1999)
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SEQUENCE 174 AA; 18337 MW;
                                                                        01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 10-MAY-2005 (TrEMBLrel. 30,
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NCBI_TaxID=487;
P95343 NEIGO PRELIMINARY;
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                                                                        01-MAY-1997
01-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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"Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF
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Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales;
Neisseriaceae, Neisseria.
NCI TaxID=487;
                                                                                                                                                                                                                                                                                                             Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 174;
                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
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                            SMR; QRR16; 20-174.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0015280; P:porin activity; IEA.
InterPro; IRF003394; Porin_opacity.
Pfam; PF02462; Opacity; 1.
SEQUENCE 174 AA; 18355 MW; ECF6F38B9286800E CRC64;
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EMBL; AR17576; AAD53279.1; -; Genomic_DNA.

HSSP; Q9RP17; 1P4T.

GO; GO:0016020; C:membrane; IEA.

GO; GO:001528; P:porin activity; IEA.

InterPro; IFR003394; Porin_opacity.

Ffam; PF02462; Opacity; 1.

SEQUENCE 174 AA; 18357 MW; 0205AAIDAIB7F005 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                         Score 852; DB 2;
Pred. No. 2.2e-67;
1; Mismatches 3;
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97.1%; Pred. No. 7.3e-67;
ive 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
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                                                                                                                                                                                                                                                                                                             98.2%; Score 852;
97.7%; Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 97.7
Matches 170; Conservative
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Q9RP18;
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                                                                                                                                                                                                                                                                                                             Query Match
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P95343_NEIGO
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RESULT: 8

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Gaps

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8; Indels

Length 174;

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Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.; "Bactericidal and cross-protective activities of a monoclonal antibody directed against Neisseria meningitidis NspA outer membrane protein."; Infect. Immun. 67:4955-459(1999).
EMBL; US2067; AAB41579.1; -; Genomic_DNA.
121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                  Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Outer membrane protein precursor.
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O65RV6 MANSM PRELIMINARY;
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Lewis L.A., Gillaspy A.F., McLaughlin R.E., Gipson M., Ducey T.F.,
Combey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,
Song L., Lin S., Yuan X., Najar F., Zhan M., Ren Q., Zhu H., Qi S.,
Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;
The complete genome sequence of Neisseria gonorrhease.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; ARO4956; AAMR88986.1; -; Genomic_DNA.
InterPro: IPR003334; Porin_opacity.
Fram; PP02462; Opacity; 1.
Complete protecome.
SEQUENCE 175 AA; 18478 MW; 44C05922D87FACF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                      1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSIGSAKGFSPRISAGYRINDLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                     95.0%; Score 824.5; DB 2; Length 175; 95.4%; Pred. No. 5.9e-65; ive 0; Mismatches 7; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
NCBI_TaxID=242231;
                                                                                                                                                                                                     SEQUENCE 175 AA; 18572 MW; DIEA8F2FF5CC2FEA CRC64;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
HSSP, Q9RP17; 1P4T.
SMR; P95371; 20-175.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0015288; F:porin activity; IEA.
InterPro; IPR003394; Porin_opacity.
PF02462; Opacity; 1.
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OrderedLocusNames=NGO0233;
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QSFA01;
                                                                                                                                                                                                                                                                                  Best Local Similarity 95.4
Matches 167; Conservative
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Best Local S
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05FA01 NET
10 G5FA0
AC G5FAC
DT 10-M
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RESULT 12 Q65RV6\_MANSM

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60 RFAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDL---- 114
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A Kim C.H., Jeong H., Hur C.G., Kim J.J.;

Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,

Kim C.H., Jeong H., Hur C.G., Kim J.J.;

"The genome sequence of the capnophilic rumen bacterium Mannheimia succiniciproducens.";

"The genome sequence of the capnophilic rumen bacterium Mannheimia succiniciproducens.";

In Nat. Biotechnol. 22:1275-1281 (2004).

R EMBL; ARO16827; ARUJ3934.1; -; Genomic_DNA.

GO; GO:0015288; F:porin activity; IEA.

R OO: GO:0015288; F:porin activity; IEA.

R Dfam; PF02462; Opacity; 1.

R Pfam; PF02462; Opacity; 1.

Complete proteome; Hypothetical protein.

Complete proteome; Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKKTLLAIIAALAMVSAAQA----NVYVEGNAGYSKIKSGEVSDHRFSPNVALGYDTGDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 -GGSDSFSQT---SIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGBLSVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKALATLI-ALALPAAALABGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDL
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EMBL; AR016877; AA037768.1; -; Genomic_DNA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0015288; F:porin activity; IEA.

InterPro; IPR003394; Porin_opacity.
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
35-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein:
OrderedLocusNames=MS1697;
Mannheimia succiniciproducens (strain MBEL55E).
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.0%; Score 303.5; DB 2; Length 177;
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
OrderedLocusNames=M$1161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 40.2%; Pred. No. 8.1e-19; Matches 74; Conservative 25; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=221988;
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S9 AMRLALDYTHYGKFSGTSYFGVNQKEHVSTKIYGLGLSAFYDFNINSVLKPYVGMRLASN 118
                                                                                                                                                                                                                                74 PRVSVGYDFGGWRIAADYASYRKWKESNSSTKKVTEDIADNYKETKTEHQGNGSFHAASS 133
                                                                                                                                                                                                                                                                              IGASAIYDFDTQSPVKPYLGARLSLNR------116
                                                                                                                                                                                                                                                                                                        DLRFAUDYTRYKNYKAPS-----TDFKLYSIGASAIYDFDTQSPVKPYLGARLSLN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 RASVDLGGSDSF---SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGE 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 LFSSAAQAASEDSGHGPYYVQADLAYAAERITHDYPKATGANNTSTVSDYFRNIRAHSIH 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 MKK---SLLVLAIGALCSLTASANFYVQGDLGVAKTKFSSYSEMNKTNIVPNVSVGYDLG
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                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-PM70;
MEDLINE-21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
May B.J.; Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460.3465 (2001).
EMBL; AE006143; AAK03109.1; -; Genomic_DNA.
                                             78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=opa; OrderedLocusNames=PM1025;
Parfeurella multocida.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                             ---KASSSLGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 186;
  Length 256;
                                             IndelB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                               64;
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28.5%; Score 247; DB 2; 28.3%; Pred. No. 1.3e-13; ive 33; Mismatches 64
                                                                                          8 LIALALPAALAEGASGFYVQADAAHA-----
                                                                                                                                                                                   48 PRISAGYRINDLRFAVDYTRYK-----
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0015288; F:porin activity; IEA.
InterPro; IPR003394; Porin_opacity.
Pfam; PF02462; Opacity; 1.
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Q9CM19;
                                               Conservative
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                   Best Local Similarity
Matches 69; Conserv
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                                             69;
                                                                                                                                                                                                                                                                              83
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                   83 ISAGYDFGDIRLAVDYSHIGKAKDHYTLFRGEQWETSGSTSVETNSFGISAIYDFNLNTS 142
                                                                                                                                                                                                           50 ISAGYRINDLRFAVDYTRYKNYK------APSTDFKLYSIGASAIYDFDTQSP 96
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawula T.H., Aho B.L., Barritt D.S., Klapper D.G., Cannon J.G.; "Reversible phase variation of expression of Neisseria meningitidis class 5 outer membrane proteins and their relationship to gonococcal proteins II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99129089; PubMed=9467908;
Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecek B.,
Heckels J.E., Cannon J.G., Achtman M.;
"Recombinational reassortment among opa genes from BT-37 complex
Neisseria meningitidis isolates of diverse geographical origins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92157869; PubMed-1787795; Aho B.L., Dempsey J.A., Hobbs M.M., Klapper D.G., Cannon J.G.; Characterization of the opa (class 5) gene family of Neisseria
                                                                                                                                          40;
                                                                                          29.5%; Score 256; DB 2; Length 226; 35.1%; Pred. No. 1.7e-14; ive 26; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                   1 MKKALATLIALALPAALAEGAS-GFYVQADAAHAKASSSLGSAKG-
                       Complete proteome; Hypothetical protein.
SEQUENCE 226 AA; 25460 MW; 106C558F9B4C1504 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 AA; 28335 MW; 9D41C6079C6DD13F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAY-1997 (TrEMBLrel. 03, Last sequence update) 01-WAR-2004 (TrEMBLrel. 26, Last annotation update) Opacity outermembrane protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ź
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Mol. Microbiol. 5:1429-1437(1991).
Mel. Wicrobiol. 5:1429-1437(1991).
Mol. Microbiol. 5:1429-1437(1991).
PIR; B60119; B60119.
PIR; S77737; S77737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NYIGKVNTVKNVRSGELSVGVRVKP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18SP, Q9RP17, 1P4T.
30, GO:0016020, C:membrane; IRA.
30, GO:0015288; F:porin activity; IEA.
InterPro; IRR003394; Porin_opacity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01,
  Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02462; Opacity; 1.
                                                                     Query Match
Best Local Similarity 35.11
Best Local 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q51124_NEIME PRELIMINARY;
Q51124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
Pubmed=3123389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Z4197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=opa;
                                                                                                                                                                                                                                                                                                                                                                                                                      143
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SEQUENCE
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10 51124 NBI
10 51124 NBI
10 5112
AC 05112
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57

Search completed: January 11, 2006, 15:21:28 Job time : 163 secs



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January 11, 2006, 15:16:52; Search time 45 Seconds (without alignments) 319.679 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                - protein search, using sw model
                                                                                                OM protein
                                                                                                                                            Run on:
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US-10-650-123-2 868 Title: Perfect score:

1 MKKALATLIALALPAAALAE......VNTVKNVRSGELSVGVRVKF 174 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

572060 572060 segs, 82675679 residues Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Issued\_Patents\_AA:\*
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*
4: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		٠			SUMMARIES	
Result No.	Score	Query Match	Length	DB	αı	Description
	898	100.0	174	7	US-08-913-362-2	Sequence 2, Appli
7	854	98.4	174	7	-08	6
٣	838.5	96.6	175	~	US-08-913-362-30	Sequence 30, Appl
4	825	95.0	174	7	US-08-913-362-8	ω,
ហ	824.5	95.0	175	~	US-08-913-362-4	4
9	135	15.6	170	Н	US-08-127-499A-20	20,
7	135	15.6	170	Н	US-08-482-847-20	20,
80	133	15.3	25	~	US-08-913-362-26	
6	113.5	13.1	96	7	US-09-540-236-2245	2245
10	109.5	12.6	187	~	US-09-489-039A-13699	
11	104.5	12.0	384	7	US-09-543-681A-7922	Sequence 7922, Ap
12	93	10.7	190	7	US-09-543-681A-7684	
13	92.5	10.7	261	7	US-09-252-991A-19759	19759,
14	89.5	10.3	186	~	US-09-540-236-2792	
15	89.5	10.3	385	~	US-09-489-039A-7451	Sequence 7451, Ap
16	88.5	10.2		~	US-09-164-714-7	7,
17	88.5	10.2		~	US-09-336-447A-3	m
18	88.5	10.2		~	US-09-952-267B-3	m
19	88	10.1		Н	US-08-457-997B-2	•••
20	88	10.1	359	~	US-08-467-722A-2	'n
21	88	10.1	359	7	US-09-451-184-2	•••
22	88	10.1	397	7	US-09-902-540-16267	• •
23	88	10.1	610	7	US-09-336-447A-11	٠.
24	88	10.1	610	~	US-09-952-267B-11	11,
25	88	10.1	624	~	US-09-336-447A-7	7
26	88	10.1	624	~	US-09-952-267B-7	7
27	88	10.1	889	~	US-09-336-447A-15	15,

DB 2; Length 174;

100.0%; Score 868;

Query Match

28	88	10.1	889	7	US-09-952-267B-15		15, Appl
29	87.5	10.1	708	N	US-09-336-115C-2		Appli
30	87	10.0	16		US-08-913-362-15	Sequence 15,	, App.
31	87	10.0	200		US-09-325-932A-149	Sequence 149,	9, Apr
32	98	6.6	512		US-09-059-584-57	Sequence 57	, App]
33	85.5	6.6	238	7	US-09-902-540-12284	Sequence 12:	284, 7
34	85.5	6.6	487		US-09-328-352-5331	Sequence 533	5331, Ag
35	82	9.6	268	4	PCT-US95-13749-5	Sequence 5,	5, Appli
36	84.5	9.7	643	7	US-09-328-352-5146	Sequence 51	5146, Ag
37	84	7.6	351	7	US-09-252-991A-30094	Sequence 30(	30094, 7
38	83.5	9.6	721		US-09-328-352-7781	Sequence 778	7781, AE
39	83	9.6	364		US-09-418-980-8	Sequence 8,	Appli
40	83	9.6	364	7	US-09-809-665A-151	Sequence 151,	1, Apr
41	83	9.6	364		US-09-506-078-45	Sequence 45	45, App]
42	82	4.6	172	N	US-09-902-540-14682	Sequence 140	14682, 7
43	82	9.4	433	-	US-08-883-515-2	Sequence 2,	Appli
44	82	9.4	433	7	US-09-770-509-27	Sequence 27	, App]
45	82	4.6	512	7	US-09-059-584-56	Sequence 56	_

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# ALIGNMENTS

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WESCUL:

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Sequence 2, Application US/08913362

Sequence 2, Application US/08913362

Sequence 2, Application US/08913362

Sequence 2, Application

SEGUENCE CORRESPONDENT:

APPLICANT: Hamel, Desee

APPLICANT: Hamel, Clement

TITLE OF INVENTION: PROTEINABE K RESISTANT SURFACE PROTEIN

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES:

ADDRESSER: ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSER: FOLEY & Lardner

STARET: D.C.

CONTRY: USA

ZIP: 20007-5109

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: Deseart PROSS/MENT:

COMPUTER: Deseart POLES/MENT:

COMPUTER: DESEARCH POLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-404-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 20,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-913-362-2
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TOPOLOGY:
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Query Match
Best Local Similarity
Matches 170; Conserv
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                                                                                                                                                 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                            61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                          1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                             1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSIGSAKGFSPRISAGYRINDLR
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                          0; Gaps
                                                                                                                                                                                                                                      121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                              121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OP SEQUENCES: 30
CORRESPONDENCE 330
ADDRESSE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.4%; Score 854; DB 2; Length 174; 98.3%; Pred. No. 2.5e-91; ive 0; Mismatches 3; Indels
                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: U.S. A. C. COURTRY: U.S. A. C. COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Batentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
PILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
PILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATFORNEY/AGENT INPORMATION:
NAME: Bent. Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELEPPAK: (2021672-5309
TELEPPAK: (2021672-5309
  ; Pred. No. 5.9e-93; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3000 K Street, N.W., Suite 500 CITY: Washington COUNTY: D.C.
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08913362
Patent No. 6287574
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 174 amira
100.001
                      Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.3
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-913-362-6
  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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US-08-913-362-6
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61 PAVDYTRYKNYK-APSTDFKLYSIGASALYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 119
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61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                         SQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

PRIOR APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MR-1995

PRIOR APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-MR-1995

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-MR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REGISTRATION NUMBER: 29,768

REFERENCE/COCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 838.5; DB 2;
Pred. No. 1.6e-89;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Weahington STATE: D.C. CUNTRY: USA ZIP: 2007-5109 COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                               Sequence 30, Application US/08913362
Patent No. 6287574
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: OF NEISSER
TITLE OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 904136
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
121 FSQTSXGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 SKTSAGLGVLAGVSYAVTPNVDLDAGYRYNYVGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                             | Sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 825; DB 2; Length 17.
Pred. No. 6.1e-88;
2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 10-MAC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUTCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
18-08-913-362-4
'Sequence 4, Application US/08913362
; Patent No. 6287574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%;
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 174 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (202) 672-5399
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MOLECULE TYPE: protein
US-08-913-362-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
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Best Local Similarity
                                                                                                                                                                        US-08-913-362-8
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61 PAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKKALATLIALALPAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 FSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/08127499A
Sequence 20, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALEXTNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 175;
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                                                                                                                                                                                                                                                                                                          CUMPRY: USA

ZIP: 2007-5109

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMFUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

PILING DATE: 13-NOV-1997

PRIOR APPLICATION NUMBER: US 08/406,362

PILING DATE: 17-MAR-1995

PRIOR APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INPORMATION:
NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REPERSENCE/DOCKET NUMBER: 29,768

REPERSENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION: NEORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 95.0%; Score 824.5; DB 2; Best Local Similarity 95.4%; Pred. No. 7e-88; Matches 167; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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US-08-127-499A-20
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46 FSPRISAGYRINDLRFAVDYTRYKNY------
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 51916/104/INBI
TELECHOME: (202) 672-5300
TELEFROM: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 26.3%; Prec. no.
Watches 41; Conservative 20; Mismatches
                                                                                                                                                                                                                                             TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY:
US-08-482-847-20
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APPLICANT: SHARMA, Lawrence Rajendra
APPLICANT: SHARMA, Lawrence Rajendra
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Sulte 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 ATLIALALPAAALAEGASGFYVQADAAH------AKASSSLGS-----AKG 45
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                                                                                                  COMPUTAT: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT: Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAK: (202) 672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD 113
                         : 3000 K Street, N.W., Suite 500 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 PSPRISAGYRINDLRFAVDYTRYKNY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-08-482-847-20
; Sequence 20, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
         Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown US-08-127-499A-20
                                                                                               USA
      ADDRESSEE:
                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
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75 IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
                                                                                                                                                                                                                                          ----KAPSTDFK 79
                                                                                                                          6 ATLIALALPAPALAEGASGFYVQADAAH-----AKASSSLGS----AKG
                                                                                                                                                                             15 SSLLFSSAAQAASEDRRSPYYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAHS
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUS-01-362-26

1 Sequence 26, Application US/08913362

1 Sequence 26, Application US/08913362

2 Sequence 26, Application US/08913362

3 Patent No. 6287704:

3 APPLICANT: Brodeur, Bernard R

APPLICANT: Hamel, Josee

APPLICANT: Hamel, Josee

APPLICANT: Hamel, Josee

APPLICANT: Hamel, Josee

APPLICANT: About, Clement

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESSED NOBERS: 300

CORRESSED FOLGY & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STRATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: TIEM FC Compatible

COMPUTER: TIEM FC Compatible

COMPUTER: TIEM FC Compatible

COMPUTER: TIEM FC COMPATA: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/406,362

FILING DATE: 13-NOV-1997

PRIOR APPLICATION NUMBER: US 60/001,983

FILING DATE: 17-MAR.1995

PRIOR APPLICATION NUMBER: US 08/406,362

ATTORNEY APPLICATION NUMBER: US 08/406.362

ATTORNEY APPLICATION NUMBER: US 08/406.362

REGISTRATION NUMBER: 29,768
                                                                   48;
15.6%; Score 135; DB 1; Length 170; 26.3%; Pred. No. 1.4e-07;
                                                                47; Indels
                                                                                                                                                                                                                                                                                                                                                              80 LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD 113
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
APPLICANT: GARY BRETON
TITLE OF INVENTION: UOLGEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIJ
TITLE OF INVENTION: UOLGEIC ACID AND THERAPEUTICS
FILE REPERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US (99/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
RICHARD APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7684, Application US/09543681A

Sequence 7684, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION:
DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 2709.1002-001

CURRENT PELLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706
                            7;
                                                                                                                                                                                    65 DGDSVGLGAGYNFNLGPF------LMTLGGKAVYLNPKDGDEGYAIAA 106
                                                                                                                                                                                                                                                    100 YLGARLSLNRASVDLGGSDSFSQTSIGLGV-----LTGVSYAVTPNVDLDAGYRY-NYI 152
                                                                                                                                                                                                                                                                           80 KDQIGAGAPAGYQYNQYLGFELGYDWLGRMAYKGSYNNGAFKAQGIQLTTKLSYPVMDDL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 KPY--LGARL-----SLNRASVDLGGSDSFSQTSIGLGVL--TGVSYAVTPNVDLDAG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 MKK---TAIALAVAVAAFATAAQAAPKDNTWYTGGKLGWSQYQSTGNNWDGVNIGNGSTH 79
                                                                        44
                                                                                                  45 -GFSPRISAGYRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASAIY----DFDTQSPVKP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 SPRIS----AGYRIND---LRFAVDYTRYKNYKAPSTD--FKLYSIGASAIYDFDTQSPV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKALATLIALALPAAALAEGASG-----FYVQADAAHAKASS-----SLGSAKGF
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 384;
                            Indels
                                                                        1 MKKALATLIA--LALPAALAEGASGFYVQADAAHAKASSSLGSAK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
  1 Similarity 25.2%; Pred. No. 0.00015; 51; Conservative 26; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.0%; Score 104.5; DB 2; 26.1%; Pred. No. 0.0017; ive 27; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 YRY-NYIGKVNTVKNVR--SGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 YOWINNIGDKGTL-NARPDNGMLSVGVAYRF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7922, Application US/09543681A Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                               153 GKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                       166 GKDGNRDNTLADGAYAGVNFRF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 26.1%
Matches 55; Conservative
Best Local Similarity
Matches 51; Conserv
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US-09-543-681A-7684
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APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARTITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT PILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2245
LENGTH: 98
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Patent No. 6610836

GENERAL INFORMATION:
APPLICAPT: Gary Breton et. al
APPLICAPT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CURRENT PAPLICATION NUMBER: US 409489,039A
CURRENT FILING DATE: 1099-01-29
RUNBER OF SEQ ID NOS: 14342
SEQ ID NO 13699
LENGTH: 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                     Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                ch 15.3%; Score 133; DB 2; I
1 Similarity 100.0%; Pred. No. 1.4e-08;
25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.1%; Score 113.5; DB 2
37.9%; Pred. No. 1.9e-05;
tive 13; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.6%; Score 109.5;
       047998/0128
                                                                                                                                                                                TYPE:
TOPOLGGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PAVDYTRYKNYKAPSTDFKLYSIGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 2245, Application US/09540236
Patent No. 6673910
  REFERENCE/DOCKST NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEPAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Klebsiella pneumoniae
                                                                                         TELEX: 904136
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acide
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.19
Best Local Similarity 37.99
Matches 22; Conservative
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US-09-540-236-2245
                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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US-09-489-039A-13699
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Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                    57 N-DLRFAV-------DYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGA- 103
                                                                                                                                                                                                                                                                                                                             66 BFDNQWGMIGSFVYTHQGYDY-HWNSRKIGSIDLDYYSLAAGPVYRFNDYISAYGLVGVA 124
                                                                                                                                                                                                                                                                                                                                                                               104 ----RLSLMRASVDLGGSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVK 159
                                                                                                                                                                                                                                                                                                                                                                                               63 KALKTLFIATALLGSAAGVQAADNFV--GLTWGETSNNIQKSKSLNRNLNSPNLDKVIDN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TGTWGIRAGOQFEQGRY---YATYENISDISSGNKIRQ--QNLLGSYDAFLPIGDNNTKL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 YLGARLSLARASVDLGGSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRY------ 149
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                                                                                                                                                                                                                                                    3 KALATL-IALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGF----SPR-----49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 ----ISAGYRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPV----KP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.7%; Score 92.5; DB 2; Length 261; llarity 23.4%; Pred. No. 0.024; Conservative 29; Mismatches 84; Indels 4
                                                                                                                                                  10.7%; Score 93; DB 2; Length 190; 26.0%; Pred. No. 0.013; ive 32; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 PHGGNKLGSLDLHS---SSQFYLGANYKF 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 ----NYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Pseudomonas aeruginosa
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19759
LENGTH: 261
                                                                         TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                       50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 NVRSGELSVGVR 171
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179 -VGTWMLGLGYR 189
               NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7684
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Matches 49; Conserv
                                                                                                                                                                     Best Local Similarity
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US-09-252-991A-19759
                                                                                                            US-09-543-681A-7684
                                                       LENGTH: 190
                                                                                                                                                      Query Match
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RESULT 14

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Patent No. 6673910
GRNERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
SEQ ID NO 2792
LENGTH: 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7451, Application US/09489039A
Sequence 7451, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Brecon et. al
APPLICANT: Gary Brecon et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREDMONIAE FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR PLING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7451
LENGTH: 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 SLARASVDLGG-----SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SDSFSQTSIGLG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KALATLIA-----LALPA-AALAEGASGF---YVQADAAHAKASSSLGSAKGFSPRISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
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CORGANISM: M.catarrhalis
US-09-540-236-2792
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Search completed: January 11, 2006, 15:23:15 Job time : 46 secs



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	Description	AF175680 Neisseria	AF175682 Neisseria	AF175683 Neisseria	CQ786532 Sequence	CQ814512 Sequence	US2066 Neisseria m	AR167414 Sequence	AF175678 Neisseria	Continuation (7 of	AX044030 Sequence	U52068 Neisseria m	AR167416 Seguence	AL162754 Neisseria	AF175677 Neisseria	AF175679 Neisseria	AF175676 Neisseria	AF175681 Neisseria	AY157539 Neisseria
SUMMARIES	ΩI	AF175680	AF175682	AF175683	CQ786532	CQ814512	NMU52066	AR167414	AF175678	AE002098 06	AX044030	NMU52068	AR167416	NMA3 22491	AF175677	AF175679	AF175676	AF175681	AY157539
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عد ا	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.4	99.4	99.4	98.8	98.8	98.8	98.5	98.5	98.2	98.2	95.7
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US2069 Neisseria g AK68533 Sequence AR167410 Sequence AR167420 Sequence US2067 Neisseria m AR167415 Sequence Continuation (3 of COR110 Sequence CO771466 Sequence CO771466 Sequence CO771466 Sequence CO771466 Sequence COR1100010 (17 o AP006604 Cyanidios AK106151 Oryza sat CONTINUATION (106 AP004225 Oryza sat AR067529 Oryza sat AR067530 Oryza sat AR067530 Oryza sat AR067530 Oryza sat AR10953 Oryza sat AR10953 Oryza sat CONTINUATION (51 o CONTINUATION (52 o	meningitidis strain M986 surface protein A (nspA) gene, cds.  1 GI:582535  meningitidis strain M986 surface protein A (nspA) gene, cds.  1 GI:582535  meningitidis meningitidis meningitidis meningitidis cae, Noisesria.  1-40.525  Tah, S. and Granoff, D.M. es in Surface Expression of Neisserial Surface Protein A seria meningitidis Group B strains 1 to 525  2 to the meningitidis "  2 to the meningitidis "  2 to the meningitidis "  3 to the meningitidis "  4 to the meningitidis "  4 to the meningitidis "  4 to the meningitidis "  5 to can in dia "Add 18 to the meningitidis "  5 to can in dia "Add 18 to the meningitidis "  5 to can in dia "Add 18 to the meningitidis "  5 to con attain "  6 to the meningitidis "  6 to the meningitidis "  7 to the meningitidis "  7 to the meningitidis "  8 to the meningitidis "  9 to the meningitidis "  9 to the meningitidis "  1 to 525  1 to 525  1 to 525  1 to 525  2 to the meningitidis "  3 to the meningitidis "  4 to the meningitidis "  5 to the meningitidis "  5 to the meningitidis "  5 to the meningitidis "  6 to the meningitidis "  8 to the meningitidis "  9 to the meningitidis "  9 to the meningitidis "  1 to the meningitidis "
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GFSPRISASTRINDLRFAVDYTRYKAYKAPSTDFKLYSIGASAIYDPDTQSPYKPYLG
ARLSLARASVDLGGSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYKYTKTKYKNTVKN
VRSGBLSVGYRVKF.
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Neisseria meningitidis strain NGP165 surface protein A (nspA) gene,
complete cds.
AR175683
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Neisseria maningitidis
Neisseria maningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.

1 (bases 1 to 525)
Noc. G.R., Tan,S. and Granoff,D.M.
Differences in Surface Expression of Neisserial Surface Projamong Neisseria meningitidis Group B strains
Infect. Immun. (1999) In press
Infect. Jan,S. and Granoff,D.M.
Moe,G.R., Tan,S. and Granoff,D.M.
                                                                                                                                                                                                                              Length 525
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; Pred. No. 1.2e-89;
0; Mismatches 0;
                /gene="nspA"
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/transf_table=11
/producf="surface_protein A"
/protein_id="AAb53285.1"
/db_xref="GI;5825541"
                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 525; Conservative 0;
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Neisseria meningitidis strain NG6/88 surface protein A (nspA) gene,
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1 (bases 1 to 525)

Moc.G.R., Tan,S. and Granoff,D.M.

Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains

1 (1999) In press

2 (bases 1 to 525)

Moc.G.R., Tan,S. and Granoff,D.M.

Submitted (04-AUG-1999) Children's Hospital Oakland Research Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA

Location/Qualifiers
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Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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                                      Length 525;
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/organism="Neisseria meningitidis"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="taxon:487"
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Tommassen,J. and Weynants,V.
Refolding method
                     Betaproteobacteria; Neisseriales;
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Neisseria meningitidis
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae, Neisseria.
                                                                                                                                             1. .525
/organism="Noisseria meningitidis"
/mol_type="unassigned DNA"
/strain="6088"
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                                                                     Martin, D. and Rioux, S.
Pharmaceutical liposomal compositions coderived polypeptides or polymucleotides
Patent: WO 2004019976-A 1 11-MAR-2004;
SHIRE BIOCHEM, INC. (CA)
Location/Qualifiers
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Sequence 8 from Patent WO2004020452.
CQ814512
CQ814512.1 GI:47603711
                                                                                                                                                                                                                                                 db xref="taxon:487"
   Neisseria meningitidis
Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
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CQ814512
LOCUS
DEFINITION
ACCESSION
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/ gene="nspa"
/ codon start=1
/ transl_table=11
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/ product="surface protein A"
/ protein_id="AAD532586.1"
/ db_xref="G1:625543"
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ARLSINFASYDLGGSDSFSQTSIGLGVLTGVSYAVTPNYDLDAGYRYNTGWRYUGA
VRSGELSVGVRVKF"
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Direct Submission
Submitted (04-AUG-1999) Children's Hospital Oakland Research
Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
Location/Qualifiers
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Organism="Neisseria meningitidis"
/mol_type="genomic DNA"
/strain="NGP165"
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Neisseria meningitidis
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Matches 52
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complete cds.
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Patent: WO 2004020452-A 8 11-MAR-2004;
GlaxoSmithKline Biologicals S.A. (BE); Utrecht University (NL)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Plante, M., Cadieux, N., Rioux, C.R., Hamel, J., Brodeur, B.R. and
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Neisseria meningitidis
Sacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 830)
Martin,D., Cadieux,N., Hamel,J. and Brodeur,B.R.
Highly conserved Neisseria meningitidis surface protein conprotection against experimental infection
J. Exp. Med. 185 (7), 1173-1183 (1997)
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Neisseria meningitidis outer membrane protein gene,
US2066
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                                                                                                                  1. .525
Coganism="Neisseria meningitidis"
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/db_xref="taxon:487"
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                                                                                                                                                                                                                                                                                                                                            100.0%; Score 525; DB 6;
100.0%; Pred. No. 1.2e-89;
iive 0; Mismatches 0;
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525;
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Best Local S
Matches 525
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VERSION
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SOURCE
ORGANISM
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NMU52066
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VRSGELSYAVVRVKF"
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                                                                                                                                                                                                                       Direct Submission
Submitted (22-MAR-1996) Denis Martin, Department of Microbiology,
Submitted (22-MAR-1996) Denis Martin, Department of Microbiology,
University Laval, Unite de Vaccinologie, Laboratoire et Service
d'Infectiologie, Centre Hospitalier de l'Universite Laval, 2705
boul Laurier, Ste-Foy, Quebec GIV 4G2, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 ATGAAAAAAGCACTTGCCACACTGATTGCCCTCGCCCCCCGGCCGCCGCACTGGCGGAA
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3 (bases 1 to 830)
Cadieux, N., Plante, M., Rioux, C.R., Hamel, J., Brodeur, B.R. and
                                         Martin, D.
Bactericidal and cross-protective activities of a monoclonal antibody directed against Neisseria meningitidis NspA outer membrane protein
Infect. Immun. 67 (9), 4955-4959 (1999)
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100.0%; Pred. No. 1.1e-89;
ative 0; Mismatches 0;
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ARLSLMRASYDLGGSDFSGTSIGLGVLTGVSYAVTFNVDLDAGYRYNYIGKVNYTVKN
VRSGELSAGVRVKF"
                                                               Neisseriaceae, Neisseria.

1 (bases 1 to 525)

Moe,G.R., Tan,S. and Granoff,D.M.

Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains

Infect. Immun. (1999) In press
2 (bases 1 to 525)

Moe,G.R., Tan,S. and Granoff,D.M.

Direct Submission

Submitted (04-AUG-1999) Children's Hospital Oakland Research Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA

Location/Qualifiers
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                 Neisseria meningitidis
Neisseria meningitidis
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales;
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Organisma"Neisseria meningitidis"
/mol_type="genomic DNA"
/strain="CU385"
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Pred. No. 4.7e-89;
0; Mismatches 2.
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Nelsseria meningitidis strain CU385 surface protein A (nspA) gene,
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Unknown.
Unclassified.
I (bases 1 to 830)
Brodeur, B.R., Martin, D., Hamel, L. and Rioux, C.
Brodeur, B.R., Martin, D., Hamel, L. and Rioux, C.
Proteinase K resistant surface-protein of neisseria meningitidis
Patent: US 6287574-A 1 11(5EP-2001.)
Location/Qualifies
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Best Local Similarity 100.0%; Pred. No. 1.1e-89;
Matches 525; Conservative 0; Mismatches 0;
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                                                                                                                Sequence 1 from patent US 6287574.
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Masignani, V., Galeotti, C., Mora, M., Ratti, G., Scarselli, M.,
Scarlato, V., Rappuoll, R., Frazer, C.M. and Grandi, G.
Neisseria genomic sequences and methods of their use
Nonsoparion (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)
CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)

Location/Qualifiers

1. 349980
Ince /organism=meningitidis // Ab zref="taxon:487"
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Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
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Pred. No. 3e-89;
0; Mismatches 2; Indels 0;
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Brodeur, B.R., Martin, D., Hamel, J. and Rioux, C.
Proteinase K resistant surface protein of neisseria meningitidis
Patent: US 6287574-A 5 11-SEP-2001;
Location/Qualifiers
CTCGGCGCGCGCGCTTGAGCCTCAACCGCCTCCGTCGACTTGGGCGGCAGCGACAACCACCTTC
                                                                                                                                                                                                                                                  GTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAAAAC
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Pred. No. 1.8e-88;
0; Mismatches 4
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7codon Start=1
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7codon Start=1
7product="outer membrane protein"
7protein id="AAB41580.1"
7protein id="AAB41580.1"
7db xref="G1:1808967"
7db xr
                                                                                                                                                                NMU52068 850 bp DNA linear BCT 03-SEP-1999
NeisBeria meningitidis outer membrane protein gene, complete cds.
U52068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 TACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCCCAATCGCCCGTCAAACCGTAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (22-MAR-1996) Denis Martin, Department of Microbiology,
University Laval, Unite de Vaccinologie, Laboratoire et Service
d'Infectiologie, Centre Hospitalier de l'Universite Laval, 2705
boul Laurier, Ste-Foy, Quebec GlV 4G2, Canada
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGABABABAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAGCCTCAAGCTCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCCATCCACCGATTTCAAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCGCCGTCGATTACACGCGCTACAAAACTATAAAAGCCCCATCCACCGATTTCAAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bactericidal and cross-protective activities of a monoclonal antibody directed against Neisseria meningitidis NspA outer membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                      Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales
Neisseriaceae; Neisseria.
1 (bass 1 to 850)
Cadieux,N., Plante,M., Rioux,C.R., Hamel,J., Brodeur,B.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Neisseria meningitidis"
|mol_type="genomic DNA"
|strain="24063"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 518.6; DB 1
Pred. No. 1.8e-88;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Infect. Immun. 67 (9), 4955-4959 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:487"
/clone="pNP2205"
140. .145
196. .199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.8%;
                                                                                                                                                                                                                                                                           U52068.1 GI:1808966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 850)
Martin, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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CDS
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                                     90306
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Best Local S
                                                                                                                          RESULT 11
NMUS2068
LOCCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
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PUBMED
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TITLE
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AUTHORS
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force "NMANTO", possible ribonuclease BN, len: 408 aa; similar to SW:RBN_ECOLI (EMBL:L19201), rbn, Escherichia coli ribonuclease BN (EC 3.1.-..), fasta ascores; E(): 2.3e-28, 34.3% identity in 268 aa overlap. Longer than rbn at the C-terminus. Also similar to TR:08549 (EMBL:AF067083) Vitreoscilla sp. hypothetical protein (376 av), fasta scores; E(): 0, 45.0% identity in 33a aa overlap. Contains a region similar to NMA067), fasta scores; E(): 4.3e-08, 64.4% identity in 45 aa overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="NMA0701, possible pseudogene, len: 258 bp; shows weak similarity to part of SW:WRBA_ECOLI (EMBL:M99166), wrbA, Bscherichia coli Trp repressor binding protein (197 aa), fasta scores; E(): 0.064, 29.3% identity in 82 aa overlap. Also similar to part of TR:085450 (EMBL:AR067083) Vitreoscilla sp. Trp repressor binding protein (fragment) (124 aa), fasta scores; E(): 6.6e-14, 56.6% identity in 83
                                                                                                                                                                                                                            /codon_start=1
/trans1_table=11
/product="putative ABC transporter protein (pseudogene)"
Escherichia coli microcin transport protein (707 aa), fasta scores; E(): 2.6e-19, 53.2% identity in 111 aa overlap. Contains PS00211 ABC transporters family signature. NMA0686 may be the remainder of this pseudogene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon start=1
/transI_table=11
/product="hypothetical protein NMA0701 (pseudogene)"
complement(2755..2764)
/note="Core DNA uptake sequence: gccgtctgaa"
/label=DUS
                                                                                                                                                                                                                                                                                                                                                                                                              /note="PS00211 ABC transporters family signature"
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1376. .1385
/note="Core DNA uptake sequence: gccgtctgaa"
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/note="Core DNA uptake sequence: gccgtctgaa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (1101. .2327) /gene="NMA0700"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (1101. .2327)
/gene="NMA0700"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/transl_table=11
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/gene="NMA0701"
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                                                                                                                                                                                                                                                                                                                                              868. .912
/gene="NMA0699"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as does rbn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2444. .2453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /pseudo
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/note="NWA0698"
/note="NWA0698"
/note="NWA0698"
/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note"/note note in the soft of the note of th
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KGWPanyilvmkdgnbgnfdkiisglvleyykeddniyfsyidgggfasdscyykpei
Lygkiilnknhiininsmeknnflsedkimkgtrnmladpknkcnigtld"
                                                                                                                                                                                                                                                                                                                                                                                16-APR-2005
   Neisseria meningitidis 22491

Neisseria meningitidis 22491

Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales;

Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales;

Batteria, J. Achtman, M., James, K.D., Bentley, S.D., Churcher, C., Rlee, S.R., Morelli, G., Basham, D., Brown, D., Chillingworth, T., Davies, R.M., Davis, P., Devlin, K., Feltwell, T., Hanlin, N., Holroyd, S., Jagels, K., Leather, S., Moule, S., Mungall, K., Challingworth, T., Challingworth, M., Rajandream, M.A., Rutherford, K.M., Simmonds, M., Skelton, J., Whitchead, S., Spratt, B.G. and Barrell, B.G. Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491

L. Nature 404 (6777), 502-506 (2000)
                                                                                                                                                                                                                                                                                                                                                                                NMA3Z2491
Neisseria meningitidis serogroup A strain Z2491 complete genome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="NMA0699, pseudogene, probable ABC transporter protein, len: 336 bp; similar to C-termini of many ABC transporters e.g. TR:Q46973 (EMBL:U47048), mtfB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Notes:
Details of N. meningitidis sequencing at the Sanger Centre are available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).
Location/Qualifiers
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Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
Bequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 18A B-mail: parkhill@sanger.ac.uk
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/db_xref="UnlProt/TrEMBi:Q9JQQ2"
                                                                                                                     GTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTCAAATTCTGA
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/note="gerogroup: A"
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/gene="NMA0699"
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Parkhill, J.
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REFERENCE AUTHORS

AUTHORS REFERENCE JOURNAL

TITLE

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GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA
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/gene="nspA"
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                                                                                                                                                       2871. 3530

James-NMA0702, len: 219 aa; similar to TR:Q52925

/note="NMA0702, len: 219 aa; similar to TR:Q52925

/note="NMA0702, len: 219 aa; similar to TR:Q52925

(EMB1:Z50189), fasta scores; R(): 31-15-15, 32.7‡

identity in 205 aa overlap. Also similar to many

hacterial ypothetical proteins e.g. SW:YBAX.HAEIN

[EMB1:U32789), Hill91, Haemophilus influenzae hypothetical

protein (196 aa), fasta scores; E(): 0, 79.2‡ identity in
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GLFAAATPAREAKQKALGTLLTDSYVQQHKONLKOVONLLALDRIGNFHIRLTPNPHGK
PARIGFQGYLPI"
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6-pyruvoyl-tetrahydropterin synthases e.g. SW:PTPS_RAT
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                            uptake sequence: gccgtctgaa"
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note="Core DNA uptake sequence: gccgtctgaa"
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Pred. No. 1.1e-88;
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1778. .2787
note="Core DNA
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/gene="NMA0704"
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|gene="NMA0703"
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llarity 99.2%;
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Neisseria meningitidis

Neisseria meningitidis

Neisseria proteobacteria;

Neisseria proteobacteria;

Neisseriaceae; Neisseria.

E 1 (bases 1 to 525)

S Moo.(3.R., Tan.,S. and Granoff,D.M.

Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains

Infect. Immun. (1999) In press

E 2 (bases 1 to 525)

Moo.(3.R., Tan.,S. and Granoff,D.M.

Direct Submission

I Submitted (04-AVG-1999) Children's Hospital Oakland Research

Institute, 747 Pifty-Second Street, Oakland, CA 94609, USA

Location/Qualifiers
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Neisseria meningitidis strain BZ232 surface protein A (nspA) gene,
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Neisseria meningitidis
Bacteria; Protebbacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 525)
Moe, G.R., Tan, S. and Granoff, D.M.
Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains
Infect. Immun. (1999) In press.
2 (bases 1 to 525)
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Neisseria meningitidis strain M136 surface protein A (nspA) gene,
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                                                             Gaps
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Direct Submission
Submitted (04-AUG-1999) Children's Hospital Oakland Research
Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
Location/Qualifiers
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                                     Length 525
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Pred. No. 3.8e-88;
0; Mismatches 5; Indels
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                                  Query Match

Best Local Similarity 99.0%;

Matches 520; Conservative
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Scoring table:

Searched:

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Adi39160 Streptomy
Adi30354 Drosophil
Adi39303 Plant cony
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Adm40964 Neiseria
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Adm40960 Rice abio
Adi18790 Plant cDN
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## ALIGNMENTS

ADL13427 RESULT 1

ADL2436 ADL2436 ACL14692 ACA38418 ACA40315 AEB91807 AA199683\_04 AA199683\_04 ABQ67797

42./ ADL13427 standard; DNA; 525 BP.	427;	N-2004 (first entry)	Neisseria meningitidis H44/76 NspA gene.	Neignerial surface protein A: NspA: refolding: recombinant production;	vaccine; subunit vaccine; prevention; diagnosis; meningococcus;	invasive bacterial disease; bacteraemia; meningitis;	Neisseria gonorrhoeae; gonorrhoea; mature protein; strain H44/76;	antibacterial; gene therapy; gene; ds.	Neisseria meningitidis: H44/76.		Location/Qualifiers	1525	/*tag= b	/product= "NspA"	157	`	5852	/*tag= c	A TOURCE MACUIE MADA	WOZ004020452-A2.		K-2004.	28-AUG-2003; 2003WO-EP010085.		30-AUG-2002; 2002GB-00020197.	) GLAXOSMITHKLINE BIOLOGICALS SA. -) RIJKSUNIV UTRECHT.	The state of the s
ADL13427	ADL13427;	03-JUN-2004	Neisseria	Neisseria	vaccine;	invasive	Neisseria	antibacte	Neiseeria		Key	cos			sig_peptide		mat_peptide			WO2004020	, 6	11-MAK-2004.	28-AUG-20		30-AUG-20	(GLAX ) G (UYUT-) R	
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Database

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ADL13425 ABZ38960 ADJ83984 ABQ44816 ABQ44817

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ADL13427

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Length

Query Match

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Result

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The invention relates to an isolated refolded Neisserial surface protein a (NspA) from Neisseria meningitidis or Neisseria gonorrhoeae. The invention also relates to the method of refolding an NspA protein; an alkaline refolding buffer comprising ethanolamine and SB-12 (3-dimethyldodecylammoniopropanesulphonate) for refolding an NspA protein; a pharmaceutical composition comprising the refolding an NspA protein, a carrier and optionally one or more other Neisserial antigens; a method of preventing or treating a Neisserial infection; an antibody immunospecific correspondent of subunit vaccine for the treatment of infections characteristics which indicate that it is a potential vaccine candidate for the development of subunit vaccines for the treatment of infections caused by Neisseria meningitidis (meningococcus), which causes invasive bacterial diseases such as bacteraemia and meningitis, or Neisserial and geneses such as bacteraemia and meningitidis of Neisserial diseases such as bacteraemia and meningitidis or Neisserial diseases such as bacteraemia and meningitidis of Neisserial diseases such as bacteraemia and meningitidis of Neisseria and in the development of new antimicrobial agents, diagnostic tests and in drug screening. However, recombinantly produced proteins are frequently unable to adopt their biologically active conformations, and yields may be very low due to mis-folding and aggregation of the protein. The method of the invention provides an improved method for refolding the NspA protein, and it is possible to increase the recovery of active protein form partly purified inclusion bodies in amounts up to 100% without the need for further purification. The refolded NspA protein is useful for preparing a composition for diagnosing treating or preventing infection caused by Neisseria meningitidis or Neisseria general proverse treates meningitidis or Neisseria generaling its possible to adopt the NspA gene from Neisseria generaling its protein formation caused by Neisseria meningitidis or Neisseria me 1 ATGAAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA 60 · GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAGCCTCAAGCTCTTTA 120 GETTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCGC 180 TTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAACTT 240 61 GGGGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA 120 GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC 180 TTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAACTT 240 TACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCCCAATCGCCCGTCAAACCGTAT 300 TACAGCATCGGCGTCCGCCATTTACGACTTCGACACCCCAATCGCCCGTCAAACCGTAT 300 ATGAAAAAAGCACTTGCCACACACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA 60 Gaps New refolded NspA protein, useful for preparing a composition for diagnosing, treating or preventing infection caused by Neisseria meningitidis or Neisseria gonorrheae. ö DB 12; Length 525; Sequence 525 BP; 117 A; 186 C; 119 G; 103 T; 0 U; 0 Other; Indels 100.0%; Score 525; DB 12; 100.0%; Pred. No. 5.3e-125; . 0 0; Mismatches Disclosure, Fig 3; 62pp; English Best Local Similarity 100. Matches 525; Conservative WPI; 2004-239150/22. P-PSDB; ADL13428. 241 Query Match 121 121 181 181 241 301 셤 용 ઠે 셤 ઠે g Š 셤 ò ò

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The present invention relates to a pharmaceutical composition comprising a liposome associated with an isolated polypeptide derived from Neisseria meningitidis strain 608B, where the polypeptide is the NBA protein. The composition is useful for inducing an immune response against N. meningitidis, for preventing and/or treating N. meningitidis infection and for treating and/or preventing neisserial infection chosen from N. meningitidis, N. gonorrhoase, N. lactamica and N. polysaccharea. It is useful for treatment or prophylaxis of meningitis and meningoccaemia, in a host. The host is a mammal, preferably a human and more preferably an adult human. The present sequence is the Neisseria meningitidis strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition comprising liposome associated with isolated polypeptide or polynucleotide derived from Neisseria meningitidis strain 608B, or its fragment or analog, useful for inducing an immune response against N.
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Best Local Similarity 100.0
Matches 525; Conservative
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A proteinase K resistant surface protein has been of N. meningitidis (AAT33039 to AAT39042). The introduce fragments of antibodies can be used in prevention of infection by N. meningitidis or by humans. The antibodies may also be used diagnostically to detect antibodies meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen. DNs sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
     Neisseria meningitidis antigen, highly conserved strains - useful for prodn. of antibodies for imm diagnosis of, N. meningitidis infection.
                                                Claim 12; Fig 1; 117pp; English
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                                                                                        TACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCCCATTCGCCCGTCAAACCGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                   Proteinase K resistant N. meningitidis 22 kD surface protein.
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95US-0001983P.
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143. .667
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04-AUG-1995;
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22-DEC-1996
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                                            Query Match 100.0%; Score 525; DB 2; Length 830; Best Local Similarity 100.0%; Pred. No. 5.9e-125; Matches 525; Conservative 0; Mismatches 0; Indels
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tumouricidal immunocyte; antitumour.
                     30-MAY-2001; 2001US-00870759.
                           31-MAY-2000; 2000US-0208128P.
     Neiserria meningitidis.
                                            WPI; 2003-361759/34.
                                (TERM/) TERMAN D S.
                                               P-PSDB; ABU79079.
          352002177558-A1
                28-NOV-2002
                                      Terman DS;
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A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis in T cells and antigen presenting cells.

Disclosure; Page; 167pp; English

The invention relates to a mammalian cell receptor, useful in the creatment of cancer, which binds to tumour associated lipids and induces anergy or apoptosis in the T cells and antigen presenting cells (APCS). Also included are a mammalian cell useful in the treatment of cancer where the receptors which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (MI) a tumourcidal immunocyte population in vio in wammal (by allowing tumour associated lipids to contact immunocyte in which creeptors for immunosuppressive fatty acids, ceramides, glycolphids, phosphosphingolipids, ganglioside, sphingolipids, glycosphingolipids and protecely colpids are inactivated or clated), a construct useful in the treatment of cancer (where an adaptor protein which into the treatment of cancer (where an adaptor protein which into the treatment of cancer (where an adaptor protein which cancer (comprising a lipid raft conjugated to a superantigen), producing (MI) a tumour associated lipids are inactivated or deleted or functionally deactivated), a composition weight in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producing cancer (comprising a lipid raft conjugated to a superantigen), producing cancer (comprising a lipid raft conjugated to a superantigen), producing context for the lipids are inactivated or deleted to produce a tumouricidal part of context for the lipids are inactivated or deleted to defect or produce a tumouricidally activated oppulation, and administering the tumouricidal and mammal by allowing a tumouricidal in which receptors for the lost), producing (MI) a tumour associated or produce a tumouricidally activated or deleted or produce a tumouricidally activated or deleted or produce a tumouricidal insumosuppressive tumour associated antigens, are deleted or produce a tumouricidal insumosuppressive tumour associated antigens, are deleted or produce a tumouricidal and antimistering libid raft conjuctors or context fusion constructs with anti-tumour proteins or motifs. The present sequence encodes an anti-tumour protein which is co-administered with or incorporated into a fusion construct with a superantispen. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US patnet

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office website at "segdata.uspto.gov/sequence.html?DocID=20020177551"
                                                                                         Gape
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                                                       100.0%; Score 525; DB 8; Length 830; 100.0%; Pred. No. 5.9e-125; ative 0; Mismatches 0; Indels (
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Matches 525; Conservative
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                                                                                                                                                                                                                                      regular activation by receptors specific for lipid-based tumour associated antigen. The receptor has cytostatic and antimicrobial properties and is suitable for use in gene therapy. The receptors, methods and compositions are useful for treating a neoplastic disease or tumour (cancer), and infectious diseases. This sequence encodes Neisseria meningitidis lipopolysaccharide (LPS) to which tumour cells develop
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                                                                  New receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumor associated antigens, useful treating a neoplastic disease or tumor, and infectious diseases.
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                                                                                                                                                                Disclosure; SEQ ID NO 35; 151pp; English.
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WPI; 2003-787326/74.
P-PSDB; ADF43316.
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monoglycosylceramide or diglycosylceramide, where expression of the superantigen and the mono- or diglycosylceramide is capable of eliciting conspiration and the mono- or diglycosylceramide is capable of eliciting constitution immune response in a mammal into which the cell is introduced; (2) treating a tumor or neoplastic disease in a subject; (3) preparing a population of immunotherapeutic T or natural killer T (NKT) cells useful to treat a tumor or neoplastic disease in a subject; (4) an apoptotic cell preparation or lysate useful for treating a tumor or neoplastic disease in a subject; (4) an apoptotic cell preparation or lysate useful for treating a tumor or neoplastic disease in a subject; (4) an condensation apoptosis or lysis; and (5) a cell that has ingested to been transfected with the above apoptocic preparation or lysate, thus, cransfected with the above apoptocic preparation or lysate, thus, cransfected with the above apoptocic preparation or lysate, thus, cransfecting nucleic acid or material ingested to the immune system of methods are useful for treating tumors or neoplastic diseases. The composition of the presente a Neisseria meninglitied in classeria meninglities which induces meningococcal meningitis, which is given in the cell of this patent is not repersented in the printed appecification, but was the induced in the printed appecification, but was obtained in the present which the menunce of the present invention. Note - The sequence data for this patent is not repersented in the printed appecification, but was obtained in the present of the presen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a composition for treating a tumor or neoplastic disease in a subject. Also described: (1) a mammalian cell comprising an exogenous nucleic acid encoding a superantigen expressed in the cell, which cell also produces or expresses all alpha-anomers of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New composition for treating a tumor or neoplastic disease in a subjecomprises conjugates comprising superantigen polypeptides or nucleic acids with other molecules that produce a tumoricidal response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           obtained in electronic format directly from the USPTO web site.
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100.0%; Pred. No. 5.9e-125;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 35; 125pp; English.
                                                                                                                                                                                          08-SEP-2004; 2004US-00937758.
                                                                                                                                                                                                                                                30-AUG-2000; 2000US-00650884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                            Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                   2005-394926/40.
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TACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCCAATCGCCCGTCAAACCGTAT 300

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QQ	383 TACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCCAATCGCCCGTCAAACCGTAT 442	Dh 20158 CTCSATTTGAATGCCGGCTACGCTACAATGCGCGAAAGTCGACAAAACTCAAAAACTCAAAAAACTCAAAAAAAA
දු අ	301 CTCGGCGCGCGCTTCAACCGCGCTCCGTCGACTTGGGCGGCGCAGCGACTTC 360	481 GTCCGTTCCGGCGA
දි සි	361 AGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCCTATGCCGTTACCCCGAAT 420	0000 GICCGIICCGGCGAACIGICCGCCGGIGIGCGCGCGICAAAIICIGA
<u>ځ</u> څ	21 GTCGATTTGGATGCCGGCTACGCTACAACTACATCGGCAAAGTCAAAAAC	A814 ntin Seq
8 8	GTCCGTTCCGGCGAACTGTCCGTCGGCGTCAAATTCTGA 525	AAA81490 00 100001
Op.	623 GTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTCAAATTCTGA 667	AAA81490_03 200001 AAA81490_04 400001 AAA81490_06 60001
RESUL AAA81. Contin WP Sec WP WP WP	AAA81490 14/c  AAA81490 14/c  Continuation (15 of 15) of AAA81490 from base 1400001 (N. meningitidis B full length gen Continuation (15 of 15) of AAA81490 from base 1400001 (N. meningitidis B full length gen WP Sequence split into 15 fragments LOCUS AAA81490 Accession Aaa81490 WP AAA81490 00 100001 100000 WP AAA81490 02 200001 310000 WP AAA81490 02 300001 410000	WP AAA81490 06 600001 710000 WP AAA81490 06 70001 810000 WP AAA81490 08 800001 100000 WP AAA81490 10 1000001 1100000 WP AAA81490 11 1100001 1100000 WP AAA81490 12 1200001 13100000 WP AAA81490 13 1300001 1430608
	400001 500001 600001 700001	Query Match 99.4%; Score 521.8; DB 3; Length 110000; Best Local Similarity 99.6%; Pred. No. 1.2e-123; Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
4 4 4 4 3 3 3 3	800001 900001 1100001	Oy 1 ATGAAAAAGCACTTGCCAACTGATTGCCCTCCCTCCCGGCCGCCGCACTGGCGGAA 60
WP WP	1200001 1300001 1400001	Qy         6.1 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA         1.20           Db         90725 GGCGCATCCGGCTTTTACGTCCAAGCCGAACAGCCACACGCAAAAGCCTCAAGCTCTTTA         90666
Que Best Matt	Query Match 99.4%; Score 521.8; DB 3; Length 37668; Best Local Similarity 99.6%; Pred. No. 9.4e-124; Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	121 GGTTCTGCCAAAGGCTTCAGCCGCGG
දු දු	1 ATGAAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA 60	181
è 8	61 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCAAAAGCCTCAAGCTCTTA 120 	241 TACAGCATCGGCGTCCCCATTTACGACTTCGACACCCAATCGCCGTCAAACCGTAT 300 40545 TACAGCATCGGCGTCCGCCATTTACGACTTCGACACCCAATCGCCGTCAAACCGTAT 9048
è 8	121 GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGCTACCGCATCAACGACCTCCGC 180	301 CTCGGCGCGCCTTCAACCGCCCTCCGTCGACTTGGCCGCGCGCACCGCACCGCTC 3
දු අ	181 TICGCCGFCGATTACACGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAACTT 240 	361
දු ද	241 TACAGCATCGGCGCGCCATTTACGACTTCGACACCCCAATCGCCCGTCAAACCGTAT 300 	421 GTCGATTTGGATGCCGGCTACCGCTACACTACATCGGCAAAGTCAACTCTCAAAAAC
දු දු	301 CTCGGCGCGCGTTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCGGCAGCGACCGAC	481 GTCGTTCCGCGAACTGTCCGTCGCGTCAATTCTGA 525
ò	361 AGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGTTACCCCGGAT 420	10. C.
ብ &	20218 AGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGTTACCCGGAAT 20159 421 GTCGATTTGGATGCCGGCTACCGCTACAACTACGTCGAAAGTCAACACTGTCAAAAAC 480	RESULT 9 AAF21608/c ID AAF21608 standard; DNA; 349980 BP.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes the full length genome of Neisseria meningitidis B (NWB). The sequences in AAF2164 and AAF21607 to AAF21613 represent fragments of the NWB genomic sequence, as the sequence was too long to go in a record on it was split into 8 sequence was too long to go in a record on it was split into 8 sequences which coverlap each other at the beginning and end of each sequence by 49980 bp (1.e. the last 49980 bp of AAF21544 is repeated at the beginning of AAF21607, the last 49980 bp of AAF21569 to AAF21607 the beginning of AAF21607, and so on). AAF21545 to AAF21589 encode the Neisseria proteins given in AABS8550 to AABS853, and AAF21589 to AAF2160 represent PCR. The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. Neisseria nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria or computer storage medium or computer databases can be used in a search to computer storage medium or computer databases can be used in a search to dentify open reading frames (ORFS) or coding sequences within the NWB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scarlato V;
                                                                                                                          Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC;
Scarselli M,
                                                                                       Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tettelin H,
Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Appendix A; 692pp; English
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Masignani V, Galeotti C, Mora M,
Rappuoli R, Frazer CM, Grandi G;
                                                                                                                                                                                                                                                                                                                                                    99US-0132068P.
                                                                                                                                                                                                                                                                                                                                                                   08-OCT-1999; 99WO-US023573.
28-PEB-2000; 2000GB-00004695.
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                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR ) CHIRON CORP. (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                    Neisseria meningitidis.
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                                                                                                                                                                                                                                       WO200066791-A1.
                                                                                                                                                                                                                                                                                                                                                    10-APR-1999;
                                                       13-MAR-2001
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61 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA 120

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0; Gaps

Indels

DB 3; Length 349980;

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1 ATGAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA 90786 ATGAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA

Sequence 349980 BP; 82523 A; 82940 C; 96712 G; 87805 T; 0 U; 0 Other;

99.4%; Score 521.8; DB 3; 99.6%; Pred. No. 1.6e-123; ive 0; Mismatches 2;

Best Local Similarity 99.6 Matches 523; Conservative

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Query Match

-01-90367 90366 GTCGATTTGGATGCCGGCTACGCTACAACTACAACGTGGGCAAAGTCAAAAAGTCAAAAAAC 90307 Neisseria meningitidis antigen, highly conserved between different strains - useful for prodn. of antibodies for immunisation against, or diagnosis of, N. meningitidis infection. 480 Proteinase K reistant; Neisseria meningitidis; Neisseria gonorrhoeae, antibody; detection; probe; surface protein; ss. 620 90306 GTCCGTTCCGGCGAACTGTCCGCCGGTGTGCGCGTCAAATTCTGA 90262 Proteinase K resistant N. meningitidis 22 kD surface protein 525 481 GICCGITCCGGCGAACTGICCGICGGCGIGCGCGTCAAATTCTGA 421 GTCGATTTGGATGCCGGCTACCGCTACAACTAC Rioux C; 90426 AGCCAAACCTCCATCGGCCTCGGCGTATTGACC AGCCAAACCTCCATCGGCCTCGGCGTATTGA 90486 crceecececerraaecercaaceecece 301 CTCGGCGCGCGTTGAGCCTCAACCGCGC 90546 TACAGCATCGGCGCGTCCGCCATTTACG Neisseria meningitidis; strain Z4063. TACAGCATCGGCGCGTCCGCCATTTACC 90606 rrcccccrccarracaccccracaa Location/Qualifiers 90666 GGTTCTGCCAAAGGCTTCAGCCCGC Hamel J, TTCGCCGTCGATTACACGCGCTA AAT39041 standard; DNA; 850 BP 96WO-CA000157. 95US-00406362, 95US-0001983P. (first entry) /\*tag= a 208. .264 /\*tag= b 265. .729 208. .732 (IAFB-) IAF BIO VAC INC. /\*tag= Brodeur BR, Martin D, (revised) WPI; 1996-443187/44. P-PSDB; AAW04893. 16-OCT-2003 22-DEC-1996 15-MAR-1996; WO9629412-A1 17-MAR-1995; 04-AUG-1995; 26-SEP-1996 sig\_peptide mat peptide 361 AAT39041; 181 241 

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                             A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen, antigent fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen. DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                           447
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                                                                                                                                                                                                                                                                                                                                   GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACAAAAGCCTCAAGCTCTTTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAACTT
                                                                                                                                                                                                                                                                                Gaps
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Chlamydia trachomatis infection; Chlamydia pneumoniae infection;
protective antigen; antibacterial; vaccine; gene; ds.
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                                                                                                                                                                                                                                          Query Match 98.8%; Score 518.6; DB 2; Length 850; Best Local Similarity 99.2%; Pred. No. 2.6e-123; Matches 521; Conservative 0; Mismatches 4; Indels 0
                                                                                                                                                                                                              Sequence 850 BP; 208 A; 273 C; 185 G; 184 T; 0 U; 0 Other;
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Claim 12; Fig 9; 117pp; English
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The present invention relates to a new gram-negative bacterial bleb presenting on its surface the PorB outer membrane protein from Chlamydia trachomatis, or a protective antigen from C. pneumoniae. The invention is useful for preventing C. trachomatis or C. pneumoniae infection in a host. The present nucleic acid sequence represents a Neisseria gonorrhoeae gene as described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel gram-negative bacterial bleb presenting on its surface PorB outer membrane protein from Chlamydia trachomatis or protective antigen from Chlamydia pneumoniae, useful for preventing Chlamydia infection.
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                                                                                                                                                                                                                                                                        Verlant VGCL;
                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
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                                                                                                                                                                                                                                                                        Poolman J,
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15-AUG-2002.
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A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen, entigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. genorrhoeae in humans. The antibodies may also be used diagnostically to detect N.
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strains - useful for prodn. of antibodies for immunisation against,
diagnosis of, N. meningitidis infection.
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                                                                                                                                                                                 Proteinase K reistant; Neisseria meningitidis; Neisseria gonorrhoeae; antibody; detection; probe; surface protein; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against,
diagnosis of, N. meningitidis infection.
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                                                                                                                                Proteinase K resistant N. meningitidis 22 kD surface protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rioux C;
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
241. .765
                                                                                                                                                                                                                                                                Neisseria meningitidis; strain b2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hamel J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Fig 10; 117pp; English
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241. .297
/*tag= b
298. .762
/*tag= c
                                                   (revised)
(first entry)
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P-PSDB; AAW04894.
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04-AUG-1995;
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22-DEC-1996
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AAT39042;
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meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen. DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                GGCGCATCCGGCTTTTACGTCCAAAGCCGATGCCGCACACGCCAAAGCCTCAAGCTCTTTA 235
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                                                                                                                                ATGAAAAAGCACTTGCCGCACTGATTGCCCTCGCCCTCCCGGCCGCCGCCACTGGCGGAA 175
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                                                                                                            ATGAAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA
                                                                                         Gaps
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                                                                     Length 710;
                                                 Sequence 710 BP; 174 A; 232 C; 148 G; 156 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibacterial; infection; vaccine; gene therapy; gene; ds
                                                                                         Indela
                                                                    Score 491.2; DB 2;
Pred. No. 2.8e-116;
0; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gonorrhoeae nucleotide sequence
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                                                                     Query Match 93.6%;
Best Local Similarity 97.0%;
Matches 512; Conservative
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                                                                                                                                                                                        The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae linfection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                       New protein from Neisseria gonorrheae, useful for the manufacture of medicament for treating or preventing N. gonorrheae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 525;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 525 BP; 117 A; 188 C; 120 G; 100 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 480.2; DB 10;
Pred. No. 1.7e-113;
0; Mismatches 18;
                                                                                                                                               Disclosure; Page 371; 815pp; English
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Best Local Similarity 96.0
Matches 504; Conservative
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WPI; 2003-058415/05.
P-PSDB; ABP77991.
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CTTTACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCCCATCGCCCCGTCAAACCG

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A (Napa) from Neisseria meningitidis or Neisseria genorrhoeae. The invention also relates to the method of refolding an Napa protein; an alkaline refolding buffer comprising ethanolamine and SB-12 (3. dimethyldodecylammoniopropanegulphonate) for refolding an Napa protein; an dimethyldodecylammoniopropanegulphonate) for refolding an Napa protein; a carrier and optionally one or more other Neisserial antigens; a method of preventing or treating a Neisserial infection. Napa has considered for the Napa protein; and diagnosing a Neisserial infection. Napa has considered for the Napa protein; and diagnosing a Neisserial infection. Napa has contended by Neisserial antigens; a method of preventing or treating a meningitial exactines for the treatment of infections caused by Neisserial meningitials (meningococcus), which causes invasive bacterial diseases such as bacteraemia and meningitis, or Neisserial genorrhoeae, the causative agent of genorrhoeae, Recombinantly produced napa control also be used in the development of new antimicrobial agents, diagnostic tests and in drug screening. However, recombinantly produced proteins are frequently unable to adopt thair bologically active conformations, and frequently unable to adopt thair bologically active conformations, and fred may be very low due to mis-folding and aggregation of the protein. The method of the invention provides an improved method for refolding the Napa protein, and it is possible to increase the recovery of active protein form partly purified inclusion bodies in amounts up to 100% to without the need for further purification. The refolded Napa protein is useful for preparing a composition for diagnosing, treating or preventing infection caused by Neisseria general generia general amonalisating and infection caused. The
invasive bacterial disease; bacteraemia; meningitis;
Neisseria gonorrhoeae; gonorrhoea; mature protein; strain H44/76;
antibacterial; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New refolded Neph protein, useful for preparing a composition for diagnosing, treating or preventing infection caused by Neisseria meningitidis or Neisseria gonorrheae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated refolded Neisserial surface
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/note= "No Btart codon given"
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/tag= a
/product= "Mature NgpA"
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                                                                                                                            Location/Qualifiers
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                                                                                   Neisseria meningitidis; H44/76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-2002; 2002GB-00020197.
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P-PSDB; ADL13426.
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AACGTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTCAAATTCTGA 525
                                                                                                  Search completed: January 12, 2006, 20:20:03
Job time : 494 secs
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Score 464.8; DB 12; Length 468; Pred. No. 1.5e-109; 0; Mismatches 2; Indels 0:

88.5**%**; 99.6**%**;

Query Match Best Local Similarity 99.6 Matches 466; Conservative

present sequence represents DNA encoding the mature NspA protein fi Neisseria meningitidis H44/76 which was amplified and cloned in an example of the invention.

Seguence 468 BP; 105 A; 164 C; 106 G; 93 T; 0 U; 0 Other;

AATGTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAA

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TTCAGCCAAACCTCCATCGGCCTCTGGCGTATTGACGGGGCGTAAGCTATGCCGTTACCCCG

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us-10-650-123-1.rni

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NAME: BEHT, STEPHEN, S. 1768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 830 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Appli
Sequence 5, Appli
Sequence 29, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 33, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 1, Appli
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Sequence 15, Appl
Sequence 15, Appl
Sequence 2, Appli
                                                                                          January 12, 2006, 20:10:48; Search time 161 Seconds (without alignments) 5796.397 Million cell updates/sec
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1 atgaaaaagcacttgccac......gcgtgcgcgtcaaattctga
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-08-913-362-5

US-08-913-362-29

US-08-913-362-29

US-08-913-362-3

US-09-103-840A-2

3 US-09-103-840A-1

3 US-09-103-840A-1

3 US-09-103-840A-1

US-09-103-840A-1
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US-08-961-527-374
US-08-894-818B-15
US-09-841-553-15
US-08-894-818B-2
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Maximum Match 100%
Listing first 45 summaries
                                                              - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Sequence 6, Appli Sequence 11, Appli Sequence 2, Appli Sequence 340, Appli Sequence 342, App Sequence 342, App Sequence 343, App Sequence 3484, Ap Sequence 3484, Ap Sequence 3105, Ap Sequence 292, Appli Sequence 1233, Appli Sequence 1, Appli Sequence 7, Appli Sequence 7, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 167, Appli Sequence 167, Appli Sequence 167, Appli	ACE PROTEIN
US-08-894-818B-6 US-09-445-472-11 US-10-090-624-11 US-09-841-553-2 US-09-841-553-6 US-09-216-393B-342 US-09-216-393B-342 US-09-216-393B-343 US-09-216-393B-343 US-09-489-039A-350S US-09-489-039A-350S US-10-033-109-3 US-09-614-221A-292 US-09-614-221A-292 US-09-614-221A-292 US-09-614-221A-292 US-09-675-018B-7 US-09-675-018B-9 US-10-428-041-9 US-10-428-041-9 US-09-675-018B-9	ALICHMENTS  US/08913362  Bernard R Denis Osee 1 Osee PROTEINASE K RESISTANT SURFACE OF NEISSERIA MENINGITIDIS 30 30 SS: & Lardner reet, N.W., Suite 500 FP disk compatible PC-DOS/MS-DOS IN Release #1.0, Version #1.30 DATA: 1 US (08/913,362 Ov-1997 AR-1995 AR-1995 AR-1995 ITA: US 60/001,983 UG-1995 MATION: EN AR-1095 UG-1995
8.0 1977 3 8.0 1977 3 8.0 1977 3 8.0 1977 3 8.0 1977 3 7.9 1877 3 7.9 1867 3 7.9 1868 3 7.9 1888 9 3 7.8 1888	on John British Britis
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Best Local Similarity 99.2
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LOCATION:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA 262
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Sequence 5, Application US/08913362

Patent No. 6287574

Patent Martin, Dee18

Papticant: Hamel, Josee

APPLICANT: Hamel, Josee

APPLICANT: Hamel, Josee

APPLICANT: Hamel, Josee

APPLICANT: Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

VOMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Poloy & Lardner

STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 525; DB 3; Length 830;
Pred. No. 1.3e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 525; Du Best Local Similarity 100.0%; Pred. No. 1.3
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                          mat_peptide
200..667
                                                                                                                                                                                                                                                                                                                                sig_peptide
143..199
                                                                                                                                                                                                                                                                      143..667
                                                                                                                                                                 STRAIN: 608B
FEATURE:
                                                                                                                                                                                                                       MAME/KEY: C
LOCATION: 1
FEATURE:
LOCATION: 1
FEATURE:
LOCATION: 1
FEATURE:
LOCATION: 1
LOCATION:
LOCATION:
LOCATION:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 GGITCTGCCAAAGGCTTCAGCCCGCGATCTCCGCAGGCTACGCATCAACGACCTCCGC 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         388 TTCGCCGTCGATTACACGCGCTACAAAAACTATAAAGCCCCCATCCACGGATTTCAAACTT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Pacpy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATFORNEY/AGENT INFORMATION:
NAME: BERTE 104-AUG-1995
ATFORNEY/AGENT INFORMATION:
NAME: BERTE STEPPHEN S. 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
TELEPPAK: (202)672-5309
TELEFRAK: (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 6.8e-130;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 904136
INPORMATION POR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 850 base pairs
TYPE: nucleic acid
STRANDEDNES: double
TOPOLOGY: linear
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480
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                                                                                                                                                                                                                       61 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACAAAAGCCTCAAGCTCTTTA 120
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                                                                                                                                                                  1 ATGAAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCCGCTGGCGGAA
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                                                                                                                                          Gaps
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APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Mioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES:
ADDRESSER: FOOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
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                                                                                                           Length 810;
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                                                                                                             Score 502.6; DB 3; Length Pred. No. 1.3e-125; 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 29, Application US/08913362; Patent No. 6287574; GENERAL INFORMATION:
                                                                                                             Query Match 95.7%;
Best Local Similarity 97.3%;
Matches 511; Conservative (
                                                         mat_peptide
298..765
                 sig_peptide
241..297
US-08-913-362-29
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                                                         AGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGGTTACCCCGAAT
                                                                                 568 AGCCAAACCTCCACCGGCCTCGGCGTATTGGCGGGCGTAAGCTATGCCGTTACCCCGAAT
                                                                                                                                                                                                                                                     GTCCGTTCCGGCGAACTGTCCGTGGCGTGCGGTCAAATTCTGA 525
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ORIGINAL SOURCE:
ORGANISM: Neisseria gonorrhoeae
STRAIN: b2
FEATURE:
NAME/KEY: CDS
LOCATION: 241..765
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121 GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC 180
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                           APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Indels
                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 08/406,362
FILING DATE: US-WAR-1995
PRIOR APPLICATION NUMBER: US 00/01,983
FILING DATE: 04-AUG-1995
ATTONNEY/AGENT INPORMATION:
NAME: BEHT STEADHEN TON:
NAME: BEHT STEADHEN SP, 768
REGISTRATION NUMBER: 29,768
REFERENCE/POCKET NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 93.6%; Score 491.2; DB 3; Best Local Similarity 97.0%; Pred. No. 1.5e-122; Matches 512; Conservative 0; Mismatches 13;
                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
            Brodeur, Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 710 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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173..643
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NAME/KEY:
LOCATION:
FEATURE:
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; LOCATION:
US-08-913-362-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GGGGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCWAAAGCCTCAAGCTCTTTA 120
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                                                                                                                                                                                                                                                                                                                                                                  047998/0128
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILICH DATE: 13-00-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
FILING DATE: 17-MAR-1995
ATIONEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPANS: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: other nucleic acid;
DESCRIPTION: /desc = "consensus'
US-08-913-362-29
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US-08-913-362-3
; Sequence 3, Application US/08913362
; Betent No. 6287574
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 904136
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 528 base pairs TYPE: nucleic acid STRANDEDNESS: single
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; Sequence 2, Application US/09103840A
; Patent No. 629432B
; GENERAL INFORMATION:
; APPLICANT: FLEISCHWAN, Robert D.
; APPLICANT: FRASER, Claire M.
; APPLICANT: FRASER, Claire M.
; APPLICANT: TUSTION: TUBERCULOSIS
; TITLE OF INVENTION: TUBERCULOSIS
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REPERBENCE: 24366-20007.00
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2.
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; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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                                                                                    CCGTCGATTACACGCGCTACAAAAACTATAAAGCCCCCATCCACCGATTTCAAACTTTACA
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Best Local Similarity 44.6%;
Matches 180; Conservative
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US-09-103-840A-2
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APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT PILING DATE: 2000-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-30
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-21
PRIOR PILING DATE: 2095-12-21
PRIOR PILING DATE: 2095-12-21
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Patent No. 6677502
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Best Local Similarity 49.8%;
Matches 126; Conservative
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Rafaleki, Antoni
Orozco, Buddy
Miao, Gou-Hau
Famodu, Omolayo O.
Lee, Jian Ming
Sakai, Hajime
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GAACTGTCCGTCGGCGTGCGC 513
CURRENT FILING DATE: 1998-06-24
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Best Local Similarity 44.9%;
Matches 171; Conservative
                   NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
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US-09-103-840A-2/C
US-09-103-840A-2/C
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHANN, Robert D.
APPLICANT: FHISC. Owen R.
APPLICANT: WHITE, Owen R.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
                                                                                                                                                                                                        APPLICANT: FIRECOMMAN, KOUSTL D.
APPLICANT: FIRECOMMAN, KOUSTL D.
APPLICANT: PRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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8.7%; Score 45.6; DB 3; Length 4411529;
Best Local Similarity 44.6%; Pred. No. 0.14;
Matches 180; Conservative 0; Mismatches 224; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                        Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
APPLICANT: FLEISTHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4411529
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US-09-103-840A-1
                                                                                                           -09-103-840A-1
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OTHER INFORMATION: "n" bases at various positions throughout the
OTHER INFORMATION: represent a, t, c or g
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Pred. No. 0.2;
0; Mismatches 210; Indels 0;
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8.6%; Score 45; DB 3; Length 441
Best Local Similarity 44.9%; Pred. No. 0.2;
Matches 171; Conservative 0; Mismatches 210; Indels
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US-09-103-840A-1/C
US-09-103-840A-1/C
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
TITLE OF INVENTION: DAM SEQUENCES FOR STRAIN;
TITLE OF INVENTION: DAM SEQUENCES
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
FIRENCE OF TABLET OF T
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) OTHER INFORMATION: H37Rv
US-09-103-840A-1
TYPE: DNA ORGANISM: Mycobacterium tuberculosis
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Sequence 363, Application US/08961527

Sequence 363, Application US/08961527

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
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642 TCCCCGTCCCGCGTGTGCATCGGCCACTCCGACGACGACGACGACCTCTCTACCTCACC 701
                                                                     211 TATAAAGCCCCATCCACCGATTTCAAACTTTACAGCATCGGCGCGTCCGCCATTTACGAC 270
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Pred. No. 0.047;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                       331 TCCGTCGACTTGGGCGCCAGCGAC 354
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TELEPHONE: (301) 309-8514
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 363:
SEQUENCE CHARACTERISTICS:
LENGTH: 4483 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BTOOKSE, A ANGERE
REGISTRATION NUMBER: 36,37
REFERENCE/DOCKET NUMBER: 36,37
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STRANDEDNESS: double
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Matches 174; Conserva
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US-08-961-527-363
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US-08-961-527-363
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                                                                         126913 GGCATCTGGCTGACCGGCGACGGCTTGTCCGGCTTCAGCTCCCTGAACTCCGGCGCCGGC 426854
                                                                                                                                                                                                                    126853 AACACCGGTTTCTTCAACTCCGGCAACACCGCCAACACCGGGTTGTTCAACTCCGGCACCGGC 426794
                                                                                                                                                                                                                                                                                                                                                                   426793 AACACCGGCTTGTTCAACTCGGGCACCGGCAACGTCGGCATCGGCAACATGGGCACCGGC 426734
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APPLICANT: HOOD, ELIZABETH
APPLICANT: HOOD, ELIZABETH
APPLICANT: HOWARD, JOHN
APPLICANT: BAILEY, MICHELE
APPLICANT: GASTEL, FRANS VAN
APPLICANT: GASTEL, FRANS VAN
APPLICANT: WARD, MICHAEL
CURRENT ELICATION NUMBER: 105/981,165
CURRENT FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 5
SEQ ID NOS: 5
SEQ ID NO 4
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 TTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCGGCGACGCGACGTTCAGCCTACAAACCTCC 372
       GGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGCTTCGCCGTCGAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 ATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGTTACCCCGAATGTCGATTTGGAT 432
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                                                                                                                                               193 TACACGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAACTTTACAGCATCGGC
                                                                                                                                                                                                                                                                                                  433 GCCGGCTACCGCTACACTACATCGGCAAAGTCAACACTGTCAAAAACGTCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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8.4%; Score 44; DB 3; Length 1082;
Best Local Similarity 46.0%; Pred. No. 0.03;
Matches 149; Conservative 0; Mismatches 175; Indels
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Patent No. 6632930
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ORGANISM: Artificial Sequence
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US-09-881-165-4
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1682 GAATCTGCATCAACCAGTGCGTCCGCTTCAGCGTCAACCAGTGCGTCGGCTTCAGCGTCG 1741
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1562 GCTTCAGCAAGTACTAGTGCATCGGCTTCAGCATCGACAAGTGCGTCTGAATCGGCATCA 1621
                                                                                    1622 accacrectrocectricaccarcaaccagerecercaccarcaccacarcaccarca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gold, Larry
APPLICANT: Graig
APPLICANT: Tuerk, Craig
APPLICANT: Firthow, David
APPLICANT: Smith, Jonathan D.
TITLE OF INVENTION: Spetematic Polypeptide Evolution by Reverse Translation
FILE REFERENCE: NEX02/C1-CON
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                                                                                                                                424
                                                                                                                                                                                                                       425 ATTIGGAIGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAAAACGTCC 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 AAACTATAAAGCCCCATCCACCGATTTCAAACTTTACAGCATCGGCGCGTCCGCCATTTA
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                                                                                                                                  365 AAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGGTTACCCCGAATGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 CATCTCCGCAGGCTACCGCATCAACGACCTCCGCTTCGCCGTCGATTACACGCGCTACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Sequence OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed OTHER INFORMATION: fragments having Ncol restriction sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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45.0%; Pred. No. 0.029;
tive 0; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/197,649
CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: 07/829,461
EARLIER PILING DATE: 1992-01-31
EARLIER PILING DATE: 1992-01-31
EARLIER PILING DATE: 1991-08-01
EARLIER FILING DATE: 1991-08-01
EARLIER FILING DATE: 1990-08-02
EARLIER FILING DATE: 1990-08-02
EARLIER FILING DATE: 1990-08-02
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09197649; Patent No. 6194550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 163; Conservative
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US-09-197-649-7
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Patent No. 6420135

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                  2899 gaarcigcarcaaccagrecercecrrcaecercaaccagrecerrcecrrcaecerce 2958
                                                                                                                                                                                                                       2959 Acaagreerreeeerreageareaaceageegeereegeereageaageegaagreere
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                                                                                         365 AAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGGTTACCCCGAATGTCG 424
                                                                                                                                                                                425 ATTIGGATGCCGCCTACCGCTACAACTACATCGGCAAAGICAACACGTCC 484
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    305 GCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCGGCGCGACAGCTTCAGCC 364
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8.4%; Score 44; DB 3; Length 32768;
Best Local Similarity 47.3%; Pred. No. 0.085;
Matches 174; Conservative 0; Mismatches 185; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
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NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ. ID NO: 71:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 32768 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 CGTCCGCCATTTA-
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US-08-961-527-71
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US-08-961-527-71
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447 CAACTACATCGGCAAAGTCAACACTGTCAAAAACGTCCGTTCCGGCGAACTGTCCGTCGG 506
                                                                    374 consolidade de la contra c
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APPLICANT: Stassi, Diane L.
APPLICANT: Ruan, Xtaoan
APPLICANT: Ruan, Xtaoan
APPLICANT: Pereda-Lopez, Ana
APPLICANT: Pereda-Lopez, Ana
APPLICANT: Pereda-Lopez, Ana
APPLICANT: Pereda-Lopez, Ana
APPLICANT: Man, Xtavas, Stephan J.
ITILE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
NUMBER OF SEQUENCES: 34
CONTRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STATE: 111inois
CONFUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: LAY-1979
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: Us/08/858,003
FILING DATE: 16-ANY-1979
FILING DATE: 16-ANY-1979
REGISTRATION NUMBER: P-40,943
REGISTRATION NUMBER: 4952.US.P2
TELECOMMUNICATION INFORMATION:
NAME: DIABNICATION NUMBER: 4952.US.P2
TELEFAN: (847)-938-23137
TELEFEN:
TELEFEN: (847)-938-23137
TELEER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08858003
Patent No. 6060234
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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365 CG 366
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TOPOLOGY:
US-08-858-003-1
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US-08-858-003-1
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3: /cgn2_6/ptodata/1/pubpna/USOF_NEW_PUB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/USOF_NEW_PUB.seq:*
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8: /cgn2_6/ptodata/1/pubpna/USOF_NEW_PUB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/USOF_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                             - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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Sequence 7385, Ap Sequence 7399, Ap	"		Sequence 533, App	ρ	Sequence 550, App	Sequence 1, Appli	Sequence 140, App	Sequence 519, App		Sequence 546, App		Sequence 539, App	Sequence 2721, Ap	Sequence 518, App	Sequence 183, App	Sequence 2095, Ap	Sequence 547, App	Sequence 3729, Ap	Sequence 6989, Ap	Sequence 528, App
US-10-467-657-7385 US-10-467-657-7399	US-10-873-528-321	US-11-052-554A-519	US-11-052-554A-533	US-10-802-796-4	US-11-052-554A-550	US-11-205-109-1	US-10-858-730-140	US-11-052-554A-519	US-10-467-657-6037	US-11-052-554A-546	US-11-052-554A-529	US-11-052-554A-539	US-10-467-657-2721	US-11-052-554A-518	US-10-858-730-183	US-10-467-657-2095	US-11-052-554A-547	US-10-467-657-3729	US-10-467-657-6989	US-11-052-554A-528
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7.7	7.7	7.5	7.5	7.4	7.4	7.4	7.4	7.3	7.3	7.3	7.3	7.2	7.2	7.2	7.1	7.1	7.1	7.0	7.0	7.0
40.4	40.4	39.4	39.5	39	39	39	38.8	38.4	38.2	38.2	38.2	38	38	38	37.2	37.2	37.2	36.6	36.6	36.6
24	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

RESULT

	0;	60	120	180	240 380
US-11-103-957-91  Sequence 91, Application US/11103957  Publication No. US20050281847A1  GENERAL INFORMATION:  APPLICANT: Berthet, Francois-Xavier Jacques  APPLICANT: Lobet, Yves  APPLICANT: Lobet, Yves  APPLICANT: Vorlant, Vincent Georges Christian Louis  TITLE OF INVENTION: Vaccine Composition  FILE REFERENCE: B45.261  CURRENT FILING DATE: 2005-04-12  PRIOR PILING DATE: 2006-04-12  PRIOR PLILING DATE: 2004-02-03  PRIOR PLILING DATE: 2004-02-03  PRIOR PLILING DATE: 2001-02-08  NUMBER OF SEQ ID NOS: 108  SOFTWARE: FastSEQ for Windows Version 4.0  SEQ ID NO 91  LENGTH: 710  TYPE: DNA  ORGANISM: Neisseria gonorrhoeae  US-11-103-957-91	Query Match 95.7%; Score 502.6; DB 7; Length 710; Best Local Similarity 97.3%; Pred. No. 2.1e-125; Matches 511; Conservative 0; Mismatches 14; Indels 0; Gaps	OY 1 ATGABABAGGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCGCCGCACTGGCGGAA (D)	9y 61 GGGGGATCCGGGTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA 3	9y 121 GGTTCTGCCAAAGGCTTCAGCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC 1	OY 181 TTCGCCGTCGATTACACGCGCTACAAAAACTATAAAGCCCCATCCACCGATTTCAAACTT :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 TATTTCGGCGCGCGCTTGAGCCTCAACCGCGCTTCCGCCCACTTGGGCGGCAGCGAACCGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 ITCAGCCAAACCICCAICGGCCICGGCGIAITGACGGGCGIAAGCIAIGCCGITACCCCG
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                                                                                                                                                                                                                                                       15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 368; DB 6;
Pred. No. 2.1e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.6%;
Matches 390; Conservative
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US-11-052-554A-530/c
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                                                                                                                                                                                                                                                 561 GTCGATTTGGATGCCGGCTACGCTACTACGTCGGCAAAGTCAACACTGTCAAAAAC 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGAAAAAGCACTTGCCGCACTGATTGCCCTCGCACTCCCGGCCGCCGCACTGGCGGAA 60
                                                                                              61 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCCAAAGCCTCAAAGCTCTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2511, Application US/10467657

Publication No. US20050260581A1

GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: POXYANA Maria Rita
APPLICANT: POXYANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNAN Vega
APPLICANT: MASIGNAN Vega
APPLICANT: MASIGNAN Vega
APPLICANT: MASIGNAN Vega
APPLICANT: MONACI Elabococcal PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
FRICH FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOPTWARE: SeqWin99, version 1.04
FROM TOWNER SEQWIN99, version 1.04
                                                                                                                                                                                                                                                                                                         621 GTCCGTTCCGGCGAACTGTCCGCCGCGCGTCAAATTCTGA 665
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; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2511
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US-10-467-657-2511
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US-11-052-554A-517

US-11-052-554A-517

Publication No. US20050288866A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT APPLICATION NUMBER: US/11/052,554A

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR APPLICATION NUMBER: IN 173/DEL/2004

PRIOR PILING DATE: 2004-07-20

PRIOR PILING DATE: 2004-07-20

PRIOR PILING DATE: 2004-07-20
                                                                     APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US,11/052,554A
CURRENT PILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR PLING DATE: 2004-07-20
PRIOR FILING DATE: 2004-02-06
PRIOR FILING DATE: 2004-02-06
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                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mycobacterium tuberculosis H37Rv US-11-052-554A-530
Sequence 530, Application US/11052554A Publication No. US20050288866A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 763
SOFWARE: Patentin version 3.3
SEQ ID NO 530
LENCTH: 4617
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SOFTWARE: Patentin version 3.3
SEQ ID NO 517
LENGTH: 9903
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                                                                                                       Length 9903;
                                                                                                       Score 45; DB 7; Length 990
Pred. No. 0.012;
0; Mismatches 210; Indels
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APPLICANT: FONTANA Maria Rita

APPLICANT: POSTANA Mariagrazia

APPLICANT: MASIGNANI Vega

APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Elisabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REPERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2001-02-12
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; TYPE: DNA; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1753, Application US/10467657; Publication No. US20050260581A1; GENERAL INFORMATION:
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SOFTWARE: SegWin99, version 1.04
SEQ ID NO 1753
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US-10-467-657-1753
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                                                                                                    Query Match
Best Local Similarity 44.94
Matches 171; Conservative
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Best Local Similarity 64.79
Matches 66; Conservative
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Sequence 6237, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
ORGANISM: Neisseria gonorrhoeae
                                                                  Query Match
Best Local Similarity 47.0%;
Matches 135; Conservative
  US-10-467-657-6237
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                                                                                                         APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REPERENCE: 30853/40359A
CURRENT FILING DATE: 2005-02-07
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
FRIOR FILING DATE: 2004-03-06
SEQ ID NOS: 763
SOFTWARE: PALENTING DATE: 2004-02-06
SEQ ID: NOS: 763
SOFTWARE: PALENTING DATE: 2004-02-06
LENGTHA: 1659
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| Publication No. US20050260581A1
| GENERAL INFORMATION:
| APPLICANT: CHIRON SpA
| APPLICANT: FONTANA Maria Rita
| APPLICANT: PIZZA Mariagrazia
| APPLICANT: MONACI Elisabetta
| APPLICANT: MONACI Elisabetta
| TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
| TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
| FILE REFERENCE: 2003-08-11
| PRIOR APPLICATION NUMBER: US/10/467,657
| CURRENT FILING DATE: 2001-08-11
| PRIOR PLILING DATE: 2001-02-12
| NUMBER OF SEQ ID NOS: 9218
| SOFTWARE: SEGWIN99, version 1.04
| SEG ID NO 2385
| LENGTH: 708
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Best Local Similarity 45.3%; Pred. No. 0.013;
Matches 160; Conservative 0; Mismatches 193; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Mycobacterium tuberculosis H37Rv
                                       Sequence 552, Application US/11052554A Publication No. US20050288866A1 GENERAL INFORMATION:
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                   US-11-052-554A-552
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      Length 708;
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APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: MASIGNANI Vega
FILE REPREMENT:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT PILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR PILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 7853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 558;
Score 43.8; DB 6; Length 7
Pred. No. 0.014;
0; Mismatches 152; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7853
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LENGTH: 3990
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                                                                                                                                                                                                                                                                                                                                                       Query Match 8.2%; Score 43; DB 6; Length 687;
Best Local Similarity 62.6%; Pred. No. 0.022;
Matches 67; Conservative 0; Mismatches 40; Indels
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69.9%; Pred. No. 0.022;
iive 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI VEGA
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT PILING DATE: 2003-08-11
PRIOR PELLING DATE: 2001-02-12
                                APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
                                                                                               CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR PLILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, Version 1.04
SEQ ID NO 6237
LENGTH: 687
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; EBNEAL INFORMATION: APPLICANT: CHIRON SpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5651, Application US/10467657
Publication No. US/20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6237
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SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 5651
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US-10-467-657-5651
PIZZA Mariagrazia
MASIGNANI Vega
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Matches 58; Conservative
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Pred. No. 0.034;
0; Mismatches 285; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Length 714;
                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Indels
                              APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF ENVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILTE REFERENCE
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT APPLICATION NUMBER: US/10/467,657
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
PRIOR FILING DATE: 2001-02-12
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 6247
                                                                                                                                                                                                                                                                                                                                                                                                  8.2%; Score 43; DB 6;
62.6%; Pred. No. 0.023;
tive 0; Mismatches 4
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US-11-052-554A-520
                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6247
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Best Local Similarity 42.9%;
Matches 214; Conservative C
FONTANA Maria Rita
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Best Local Similarity 62.61
Matches 67; Conservative
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PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: Patentin version 3.3
SEQ ID NO 521
LENGTH: 4983
                                                                                                               TYPE: DNA
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                                                                   1689 CGTGCCCTTGGCACCGTTGCCGCCATCACCGCCCATGCCGCCGCGGCGCCGCTTTCCGCC 1630
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                         250 GCCCCTCCCCCATTACGACTTCGACAACCCCCTCAAACCGTAATCTCGCCCG 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3183, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FORTANA MATIA Rita
APPLICANT: PIZZA MATIAGRAZIA
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OP INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SEQ ID NO 3183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 521, Application US/11052554A Publication No. US20050288866A1 GENERAL INFORMATION:
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; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3183
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APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30653/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: IN 173/DEL/2004

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3932 ccaccritecceccecececrececerreceecececeaaaarecreeecea 3873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 CGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAACTTTACAGCATCGGCGCGT
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                                                                                                                                                                 Gaps
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                                                                                            Length 4983;
                                                                                            Score 42.6; DB 7; Length 4
Pred. No. 0.045;
0; Mismatches 204; Indels
) ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-521
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                                                                                                  8.1%;
                                                                                               Query Match
Best Local Similarity 44.7
Matches 165; Conservative
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January 12, 2006, 19:58:14 ; Search time 3281 Seconds (without alignments) 7486.504 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                         OM nucleic - nucleic search, using sw model
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US-10-650-123-1 525 1 atgaaaaaagcacttgccac......gcgtgcgcgtcaaattctga 525 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

41078325 segs, 23393541228 residues Searched:

82156650 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

9b\_est1:\*
9b\_est2:\*
9b\_htc:\*
9b\_est4:\*
9b\_est5:\*
9b\_est5:\*
9b\_est7:\*
9b\_gss1:\*
9b\_gss1:\* EST:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	. Description	CA197724 SCAGAD107	CA193415 SCCCFL100	CB654660 OSJNEC07F	CZ247380 AIAA-aaf3	CB640993 OSJNEa17F	CV152413 LS245-S.S	CB653730 OSJNEC05A	CB677411 OSJNEe14E	CF589226 EST00F06	CB671800 OSJNEe05I	CB677339 OSJNEe14C	CB677062 OSJNEe13K	CB654692 OSJNEC07G	CB665147 OSJNEd11F	CB668023 OSJNEd15K	CF278525 14ETL04	CF315326 HD04-D0	CF308604 ABF02-H	CD935542 OV.101M15	CF335206 JMT04-M	BG560231 RHIZ2_71_	CA172233 SCSFSB107
	CI	CA197724	CA193415	CB654660	0 CZ247380	CB640993	CV152413	CB653730	CB677411	CF589226	CB671800	CB677339	CB677062	CB654692	CB665147	CB668023	CF278525	CF315326	CF308604	CD935542	CF335206	BG560231	CA172233
	Length DB	622 6	626 6	787 6	743 1	591 6	665 7	9 869	725 6	741 6	759 6	762 6	775 6	778 6	782 6	842 6	561 6	644 6	525 6	9 969	530 6	558 2	655 6
٠.	Query Match	11.0	10.7	10.5	10.3	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	9.6	9.6	9.6	6.6	6.6
	Score	57.8	56.4	55.2	54.2	53.6	53.6	53.6	53.6	53.6	53.6	53.6	53.6	53.6	53.6	53.6	53.4	53.4	52.2	52	51.8	51.8	51.8
•	Result No.		7	m	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	c 19	20	21	22

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CA253038	CA231223	DN655133	CV097296	BH898151	CD219573	CD222538	CD222866				BJ748832	0 CL971648	CB643751	CK167632	BG560157	AI389106	CD223038	AW680997	BE593027	BE357605	CD463595	CW197767
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## ALIGNMENTS

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S Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 003 row: B column: 05
Seq primer: T7 Promoter Primer.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Viridiplantae, Streptophyta, Poales, Poaceae, PACCAD
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 KD were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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0; Mismatches 192; Indels
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Matches 173; Conservative
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/note=Torgan: Inflorescence at begining of development (lcm-long), Vector: pSport1; Site 1: Sal1; Site_2: Not1; An unidirectional cDNA library generated from unidirectional cDNA library generated from [Inflorescence at begining of development (lcm-long)]. CDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invirongen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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Oryza sativa (japonica cultivar-group)
Bukaryota, Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Wagnoliophyta; Liliopsida; Poales; Poaceae;
Erhartoideae; Oryzaae, Oryza.

1 (bases 1 to 787)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg, E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rearcecercerecenecedadesareacedecedecedecedecedecedadece
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAAGGCGCCATCCGGCTTTTACGTCCAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 56.4; DB 6; Length 6
Pred. No. 0.00013;
0; Mismatches 191; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
15888683
lone="SCCCFL1003E05"
host="DH108"
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Arizona Genomics Institute
                                                                                      /lab_host="DH10|
/clone_lib="FL1'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CB654660.1 GI:29658385
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Best Local Similarity 47.2%;
Matches 171; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 AT 388
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VERSION
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SOURCE
ORGANISM
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CB654660
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Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomationae; Ancylostomationae; Ancylostoma.

1 (bases 1 to 743)
Mitrava,M., McCarter,J.P., Pape,D., Ritter,E., Tsagareishvili,R., Ronko,I., Martin,J., Wylie,T., Dante,M., Meyer,R., Messina,D., Waterston,R.H., Clifton,S.W. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAAGGCTTCAGCCCGCGCATCTCCGCCAGGCTACCGCATCAACGACCTCCGCTTCGCCGT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 CGCCCCGCCCATTTACGACTTCCACACCCCAATCGCCCGTCAAACCGTATCTCGCCCC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 GCGCTTCAGCCTCAACCGCGCCTCCGTCGACTTGGGCGCGCGACAGCTTCAGCCAAAC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CICCAICGGCCICGGCGIAITGACGGCGIAAGCIAIGCCGITACCCCGAAIGICGAITI 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CB640993 591 bp mRNA linear BST 08-APR-20 OSJNEa17F21.f OSJNEA Oryza sativa (japonica cultívar-group) cDNA clone OSJNEa17F21 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ancylostome caninum genomic DNA was randomly sheared, ancylostome caninum genomic DNA was randomly sheared, end-repaired and size fractioned to enrich for 2-4 kb fragments. Genomic DNA was provided by John Hawdon (mtmjmh@gwumc.edu) at George Washington University. Sequencing by Washington University Gener, St. Louis, Mo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGATTACACGCGCTACAAAACTATAAAGCCCCCATCCACCGATTTCAAACTTTACAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Ancylostoma caninum whole genome shotgun
library (AIAAGSS 001)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAAAAAGTC 483
                                                                                                                                                                                                                                                               Washington University in St. Louis
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, 1
Tel: 314 286 1810
Pax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                          Email: nematode@watson.wustl.edu
Genomic DNA provided by John Hawdon (mtmjmh@gwumc.edu)
sequenced by Washington University Genome Sequencing Ce
Class: shotgun.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.3%; Score 54.2; DB 10; Length 743; 47.0%; Pred. No. 0.00054; arive 0; Mismatches 188; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       caninum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Ancylostoma
/mol_type="genomic DNA"
/strain="Baltimore"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db xref="taxon:29170"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="Adult"
/lab_host="GS10"
                                                                                                                                                                                                                                       Contact: Mitreva M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 167; Conservative
                                                                                                                                                                                                          Unpublished (2004)
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DEFINITION
                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                          JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                               TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="OSJNEC"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
KhoI; 6 hrs after innoculation with Rice Blast (C9240-1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGCCGCCGCACTGGCGGAAGGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCAGCGGCCATGGAGGGATACGACCGCGAGTTCTACCAGTTCACCGGACCAGCTGCGGC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAAAGCCTCAAGCTCTTTAGGTTCTGCCAAAGGCTTCAGCCCGCGCGCATCTCCGCAGGCT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCECATCAACGACCTCCCCTTCGCCGTCGATTACACGCCCTACAAAACTATAAAGCCC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATCCACCGATTTCAAACTTTACAGCCATCGGCGCGTCCGCCATTTACGACTTCGACACCC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 CCAAGAACGCCATCGCCAACATCAACGGCGTCGCCGGAAACCTGGATGGCCCGGGCCTCA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 AATCGCCCCTCAAACCGTATCTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACT 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 TCGGCTCCGGCAAGCTCGCCTTCGGCGCCACCAAGGCCGACCGCTACAACAGCGTCAACC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341 TGGGCGGCAGCGACAGCTTCAGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 rececercacaacaacaacaacaacaacaagreeraceacaccecececaacaacaaca 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTATGCCGTTACCCCGAATGTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 acaacetraacecerresesrreacaareaseseserracaacaacaecaecaaceses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480 GCGGCAACTACGGCGGCAACGGCGACGTGAAGAGCCTACTTCAACAAGTCGGTC 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                       ΥZ

    .787
/organism="Oryza sativa (japonica cultivar-group)"

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                                     Box 210088, Tucson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 55.2; DB 6; Length 7
Pred. No. 0.00029;
0; Mismatches 263; Indels
                                                                          Tel: 520 626 3967

Fax: 520 621 9288

Email: rwing@genome.arizona.edu

PCR PRimers

FORWARD: gaa aaa cga cgg cca gtg

BACKWARD: gga aac agc tat gac cat g

Plate: 07 row: F column: 21
       University of Arizona
Biological Sciences West, 448A, P.O.
85721-0088, USA
                                                                                                                                                                                                                                                               Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="OSJNEC07F21"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 10.5%;
al Similarity 44.7%;
213; Conservative
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Query Match Best Local (

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ACCESSION

caninum (dog hookworm)

Ancylostoma caninum

Ancylostoma

VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

ACCESSION

RESULT 4 CZ247380

us-10-650-123-1.rst

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Lee,J.
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                                                                                                                                                                                                                                                                                                                   ORGANISM
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AUTHORS
TITLE
                                                                                                                                                RESULT 6
CV152413
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KEYWORDS
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/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 6 hrs after innoculation with Rice Blast (Che
86061)"
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                            Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases I to 591)
Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,
Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,
Soderlund, C. and Wang, G.L.
Large-scale identification of expressed sequence tags involved in rice and rice blast fungus interaction
Flant. Ehysiol. 138 (1), 105-115 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 CGGCCGCCGCCGCACTGGCGGAAGGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 CAAAAGCCTCAAGCTCTTTAGGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 TGCAGACGGCGAGCTTCTCCCGGCCTCTCCCTCGGCGACTCCATCTGGTCCTCCCCTCCG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCGCATCAACGACCTCCGCTTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 ACCGCCGCAACGAGCCGGCCTTCGACGGCGAGTACCACCTCTCCTCCCCCTCCCCCG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATCCACCGATTTCAAACTTTACAGCATCGGCGCGCTCCGCCATTTACGACTTCGACACCC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 CCAAGAACGCCATCGCCAACATCAACGGCGTCGCCGGAAACCTGGATGGCCCGGGCCTCA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281 AATCGCCCGTCAAACCGTATCTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACT 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341 TGGGCGGCAGCGACAGCTTCAGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAA 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .591
/organism="Oryza sativa (japonica cultivar-group)"
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                                                                                                                                                                                                                                                                             Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.2%; Score 53.6; DB 6; Length 591; 44.5%; Pred. No. 0.00077; ive 0; Mismatches 264; IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: atc agc ggc cgc gat cc
BACKWARD: aat taa ccc tca cta aag gg
Plate: 17 row: F column: 21
Seq primer: atc agc ggc cgc gat cc.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEa17F21"
                                                                                                                                                                                                                                                                                                                                                                                                          Email: rwing@genome.arizona.edu
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH108"
 CB640993.1 GI:29635984
                                                                                                                                                                                                                                                                                                                                                    85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
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Isolation and chromosomal mapping of the rice clones differentially induced under abiotic stress conditions Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bioinformatics Team
National Institute of Agricultural Biotechnology, Rural Development
Administration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol type="mrNA"
/cultivar="Ilpumbyeo"
/db xref="taxon:3947"
/tissue type="caso"
/dev stage="one week old"
/dev stage="one week old"
/clone lib="Cold stressed rice cDNA library"
/note="Vector: pBlueecript SK+; Cold treatment by placing at 40C for 16 hour after growth on MS medium for one week"
                                                                                                                                                                                                                                                                                              CV152413 665 bp mRNA linear EST 08-SEP-2004
LS245-S.SEQ Cold stressed rice cDNA library Oryza sativa (japonica
cultivar-group) cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
1 (bases 1 to 665)
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                              396 ACAACGICAACGCCTTCGGGTTCAACAAGATGGGGGGTTACAACAACAGCAGCAACGGG
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                                                                                                                                                  456 GCGGCAACTACGGCGCCAACGGCGGCGACGTGAAGAGCTACTTCAACAAGTCGGTC 511

    .665
/organism="Oryza sativa (japonica cultivar-group)"

                                                                                           AAGTCAACACTGTCAAAAACGTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 Seodundon, Suwon, 441-707, Korea
Tel: 82 31 299 1663
Fax: 82 31 299 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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EST.
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Matches 212; Conservative
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 725)

Santasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,

Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,

Soderlund, C. and Wang, G.L.

Large-scale identification of expressed sequence tags involved in rice and rice blast fungus interaction

L Plant Physiol. 138 (1), 105-115 (2005)
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/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after innoculation with Rice Blast (70-15)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 09-APR-2003
221 CATCCACCGATTTCAAACTTTACAGCATCGGCGCTCCGCCATTTACGACTTCGACACCC 280
                                                                                                                                                                                                                                        227 ccaagaacccarccaacarcaacarcaacgccrcccaaaaaccrccaarcccccaaccaca 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CB677411 725 bp mRNA linear EST 09-APR-20
OSJNE214E24.f OSJNE Oryza sativa (japonica cultivar-group) cDNA
CODRE OSJNE214E24 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                281 AATCGCCCGTCAAACCGTATCTCGGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACT
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/organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nipponhare"
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
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BACKWARD: gga aac agc tat gac cat g
Plate: 14 row: B column: 24
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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/dev_stage="3 week"
/lab_host="DH10B"
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Tel: 520 626 3967
Fax: 520 621 9288
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/dev stage="3 week"
/dev stage="3 week"
/lab_host="DH10B"
/clone lib="0SNRc"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 6 hrs after innoculation with Rice Blast (C9240-1)"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (basea: 1 to 698)
Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,
Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,
Soderlund, C. and Wang, G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
              346 TCCCCGTCGACAACAACAACAACAAGTCCTACGGCGGCGCCCCAAGATCAACAACA 405
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OSJNEC05A17.f OSJNEC Oryza Bativa (japonica cultivar-group) cDNA
clone OSJNEC05A17 5', mRNA sequence.
                                                                                                            401 GCTATGCCGTTACCCCGAATGTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCA
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Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
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/mol type="mRNA"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="OSJNEC05A17"
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BACKWARD: gga aac agc tat gac cat g
Plate: 05 row: A column: 17
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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Tel: 520 626 3967
Fax: 520 621 9288
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Bmbryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Brhartoideae; Oryzae, Oryza.

1 (baes 1 to 759)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg, B., Zhou, B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
Plant physiol. 138 (1), 105-115 (2005)
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Arizona Genomics Institute
University of Arizona
Biological Giences West, 448A, P.O. Box 210088, Tucson,
85721-0088, USA
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larity 44.5%;
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Fax: 520 621 9288
                                                                                                                                                     Best Local Similarity
Matches 212; Conserv
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/mol type="mRNA"
/cultivar="Drew (a major cultivated variety in Arkansas)"
/db xref="taxon:39947"
/clone="1B193"
/tissue type="Seedling leaves"
/tissue type="Seedling leaves"
/dev gtage="16-day-old rice seedling treated by JA/BTH"
/clone_lib="Subtracted cDNA library of JA/BTH-treated rice leaf"
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                     CGGCCGCCGCACTGGCGGAAGGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACG 100
                                                                                                                                          CAAAAGCCTCAAGCTCTTTAGGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCT 160
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                                    Gaps
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10.2%; Score 53.6; DB 6; Length 725; 44.5%; Pred. No. 0.00079; ive 0; Mismatches 264; Indels
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Unpublished (2003)
Contact: Yinong Yang
Plant Pathology Department
University of Arkanasa
217 Plant Sci Bldg, Payetteville, AR 72701,
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Email: yiyang@uark.edu
Seq primer: T7.
                                  212; Conservative
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                  Similarity
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 Query Match
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Matches 21
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AUTHORS
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CF589226
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/note="Vector: pGEM-T easy; Rice seedling leaves were pretreated with 0.3 mM cyclohexmide (CHX) half an hour before treatment of 0.2 mM jasmonic acid (JA) or 0.4 mM benzothiadiazole (BTH). Both JA- and BTH-induced mRNAs were equally pooled for subtracted cDNA library construction "

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                                                                                                                                     ACCECATCAACGACCTCCGCTTCGCCGTCGATTACACGCGCTACAAAAACTATAAAGCCC
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                                               Gaps
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    Length 741;
Score 53.6; DB 6; Length 7 Pred. No. 0.00079; 0; Mismatches 264; Indels
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CB671800 759 bp mRNA linear EST 09-APR-2003 OSJNEe05117.f OSJNEe Oryza sativa (japonica cultivar-group) cDNA clone OSJNEe05117 5', mRNA sequence.

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ΑZ

 $A_{Z}$ 

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/dev_gtage="3 week"
/lab_host="DH10B"
/lofo= libl="0SJNBe"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after innoculation with Rice Blast (70-15)"
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              Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,
Stablberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A., Soderlund, C. and Wang, G.L.
Large-scale identification of expressed sequence tags involved in rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
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/organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                           Arizona Genomice Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
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Pred. No. 0.00079;
0; Mismatches 264;
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BACKWARD: gga aac agc tat gac cat g
Plate: 14 row: C column: 19
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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/clone="OSJNEe14C19"
/tissue_type="Leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rwing@genome.arizona.edu
PCR PRimers
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                                                                                                                                                                                                               Contact: Rod Wing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="OSJNEs"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
Khol; 24 hrs after innoculation with Rice Blast (70-15)"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 762)
Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,
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/mol type="mkNA"
/mol type="Nipponbare"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="GGNBe05117"
/tisue_type="Leaf"
/dev_gage="1 week"
/lab_host="DH108"
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          Email: rwing@genome.arizona.edu
PCR PRimers
FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 05 row: I column: 17
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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                                                                                                                     Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bhrhartoideae; Oryzaee; Oryza.
I (basea; Toy 75)
Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,
Stahlberg, B., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,
Soderlund, C. and Wang, G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Figure Physiol. 138 (1), 105-115 (2005)
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CB677062 775 bp mRNA 11near בטן טידיהני. CB677062 CSJNEe13KL8.f OSJNEe Oryza sativa (japonica cultivar-group) cDNA clone OSJNEe13K18 5', mRNA sequence.
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Arizona Genomica Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
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mol_type="mRN4"
cultivar="Nipponhare"
db_xref="taxon:39947"
clone="OSJNEe13K18"
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plate: 13 row: K column: 18
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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PCR PRimers
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/lab_host="DH108"
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778 bp mRNA linear EST 09-APR-2003
OSJNEC07G20.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEC07G20 5', mRNA sequence.
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/dev_stage="3 week"
/lab_host="DH10B"
/clone_llb="OSJNBC"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 6 hrs after innoculation with Rice_Blast (C9240-1)"
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases I to 778)
Jantaguriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G., Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A., Soderlund, C. and Wang, G.L.
Large-scale identification of expressed sequence tags involved in Pirce and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
336 TCCCCGTCGACAACAACAACAAGTCCTACGGCGCGCGCCCCAAGATCAACAACA 395
                                                                                                                                                                                                                                                 396 ACAACGTCAACGCCTTCGGGTTCAACAAGATGGGGGGTTACAACAACAGCAGCAACGGCG 455
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Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
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FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: G column: 20
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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Matches 212; Conservative
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Tel: 520 626 3967
Fax: 520 621 9288
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Length 782;
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  Score 53.6; DB 6;
Pred. No. 0.0008;
0; Mismatches 264;
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Plant Physiol. 138 (1), 105-115 (2005)
15888683
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PCR PRimers
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10.2%;
ilarity 44.5%;
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Fax: 520 621 9288
                      Best Local Similarity
Matches 212; Conserv
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/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after innoculation with Rice Blast (C9240-I)"
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Wiridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Enrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 782)
Jantaeuriyarat, C., Gowda,M., Haller,K., Hatfield,J., Lu,G., Stahlberg, B., Zhou, B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A., Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in Plant, Physiol. 138 (1), 105-115 (2005)
CATCCACCGATTTCAAACTTTACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCC 280
                                                                                                                                         281 AATCGCCCGTCAAACCGTATCTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACT 340
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/mol_type="mRNA"
/mol_type="mRNA"
/dultivar="Nipponbare"
/db_xref=txxon:39947"
/clone="OSJNEG11F07"
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Biological Sciences West, 448A, P.O. Box 210088, Tucson,
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BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: F column: 07
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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PCR PRimers
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/dev_stage="3 week"
/lab_host="DH108"
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Arizona Genomics Institute
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Tel: 520 626 3967
Fax: 520 621 9288
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AUTHORS
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TITLE

PEATURES

CB665147

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CB668023 842 bp mRNA linear EST 09-APR-2003 OSJNEG15K14.f OSJNEG Oryza sativa (japonica cultivar-group) cDNA clone OSJNEG15K14 5', mRNA sequence. ö Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Byermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzae; Oryza.

1 (bases 1 to 842)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in 41 CGGCCGCCGCACTGGCGGAAGGCGCATCCGGCTTTTTACGTCCAAGCCGATGCCGCACACA 100 160 221 CATCCACCGATTTCAAACTTTACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCC 280 281 AATCGCCCGTCAAACCGTATCTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACT 340 98 recabacedededrirerecesecererecesesearecearereserecerece 157 161 ACCGCATCAACGACCTCCGCTTCGCCGTCGATTACACGCGCTACAAAAACTATAAAGCCC 220 158 Acceccancadecesecricanceses and proceedations and accept acc 218 CCAAGAACGCCATCGCCAACATCAACGGCGTCGCCGGAAACCTGGATGGCCCGGGCCTCA 277 278 TCGGCTCCGGCAAGCTCGCCTTCGGCGCCCAAGGCCGACCGCTACAACAGCGTCAACC 337 341 TGGGCGGCAGCGACAGCTTCAGCCAAACCTCCGCCTCGGCGTATTGACGGGCGTAA 400 401 GCTATGCCGTTACCCCGAATGTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCA 460 38 CAGCAGCGGCCATGGAGGGATACGACCGCGAGTTCTACCAGTTCAGCGACCAGCTGCGGC 97 101 CAAAAGCCTCAAGCTCTTTAGGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCT 461 AAGTCAACACTGTCAAAAACGTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTC 516 458 ececchactracescecchacescencercenceracerricarcarerresic 513 Contact: Rod Wing Arizona Genomics Institute University of Arizona Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ ô PORWARD: gta aaa cga cgg cca gtg BACKWARD: gga aac agc tat gac cat g Plate: 15 row: K column: 14 Seq primer: gta aaa cga cgg cca gtg. Bource

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/organism="Oryza sativa (japonica cultivar-group)"

mol type="mRNA"

/cultivar="Nipponbare"
/db xref="texon:39947"

/clone="OSJNEd15K14"

/clone="OSJNEd15K14"

/dev stage="a week"
/lab_host="DH10B"

/clone="Nector: pBluescript II KS +; Site 1: EcoRI; Site 2:
KhoI; 24 hrs after innoculation with Rice Blast (C9240-I)"
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55523, A
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Sequence 36, Application US/09870759

Batent No. US20020177551A1

GRNERAL INFORMATION:
APPLICANT: TERMAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOFLASTIC DISEASE
FILE REPERENCE: 870759

CURRENT APPLICATION NUMBER: US/09/870,759

CURRENT APPLICATION NUMBER: US 60/208,128

PRIOR PILING DATE: 2000-05-30

NUMBER OF SEQ ID NOS: 166

SOFTWARE: PatentIn version 3.1

SEQ ID NO 36

LENGTH: 174
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Sequence 36, Application US/09751708A
Sequence 36, Application No. US20030157113A1
Publication No. US20030157113A1
SEMENAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
CURRENT APPLICATION NUMBER: US/09/751,708A
CURRENT FILING DATE: 2002-10-15
PRIOR PILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 166
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71651, A
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90, Appl
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100.0%; Pred. No. 4.1e-85;
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Matches 174; Conservative
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US-10-937-758A-36

Sequence 36, Application US/10937758A

Sequence 36, Application US/10937758A

Publication No. US20050112141A1

GENERAL INFORMATION:

APPLICANT TERMAN, David S

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

CURRENT APPLICATION NUMBER: US/10/937,758A

CURRENT PILING DATE: 2004-09-08

PRIOR PILING DATE: 2000-08-30
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100.0%; Score 868; I
Best Local Similarity 100.0%; Pred. No. 4.1
Matches 174; Conservative 0; Mismatches
PRIOR FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: US 60/389,366
PRIOR FILING DATE: 2002-06-15
PRIOR FILING DATE: 2002-06-15
PRIOR PLING DATE: 2002-08-28
PRIOR PLING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/415,310
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-10-01
PRIOR PLING DATE: 2002-10-02
PRIOR PLING DATE: 2002-10-03
PRIOR PLING DATE: 2003-10-03
PRIOR FILING DATE: 2003-10-03
PRIOR FILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 224
SOGTWARE: PATENTIN VERSION 3.2
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US-10-937-758A-36
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US-10-428-817A-32
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SEQ ID NO 36
LENGTH: 174
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Sequence 2, Application WS/10650123
Sequence 2, Application WS/10650123
Sequence 2, Application WS/10650123
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMT: Shire Biochem Inc.
TITLE OF INVENTION: PHARMACEUTICAL LIPOSOMAL COMPOSITIONS CONTAINING N.MENINGITIDIS I TITLE OF INVENTION: PHARMACEUTICAL LIPOSOMAL COMPOSITIONS CONTAINING N.MENINGITIDIS I TITLE OF INVENTION: PHARMACE: 14872-94
CURRENT APPLICATION NUMBER: US/10/650,123
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US 60/406,980
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 2.2
SEQ ID NO 2.2
SEQ ID NO 2.2
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US-10-428-817A-32
ISGUENCE 32, Application US/10428817A
Sequence 32, Application US/10428817A
Sequence 32, Application No. US20040214783A1
GAMERAL INFORMATION:
GAMERAL INFORMATION:
TITLE OF INVERTION:
TITLE OF INVERTION COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 38373-189118
CURRENT APPLICATION NUMBER: US/10/428,817A
CURRENT PILLING DATE: 2003-05-05
FRIOR APPLICATION NUMBER: US 60/378,988
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100.0%; Score 868; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.1e-85;
Matches 174; Conservative 0; Mismatches 0; Indels
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Local Similarity 100.0%; Pred. No. 4.1e-85;
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; ORGANISM: N. meningitidis strain 608B
US-10-650-123-2
                                                                                 ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-751-708A-36
            SOFTWARE: PatentIn version 3.1
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                                  SEQ ID NO 36
LENGTH: 174
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US-10-650-123-2
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US-10-467-534-90
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US-10-988-943-16
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TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE
TITLE OF INVENTION: DENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN
TITLE OF INVENTION: COMPLEX MIXTURES.
FILE REPERENCE: Proteomics CU2003-269
CURRENT APPLICATION NUMBER: US/10/988,943
CURRENT FILING DATE: 2004-11-15
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PATENTIN VET: 2.1
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                                          Query Match 99.5%; Score 864; DB 4; Length 17 Best Local Similarity 99.4%; Pred. No. 1.1e-84; Matches 173; Conservative 0; Mismatches 1; Indels
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99.5%; Score 864; DB 5;
Best Local Similarity 99.4%; Pred. No. 1.1e-84;
Matches 173; Conservative 0; Mismatches 1;
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i TYPE: PRT
i ORGANISM: Neisseria meningitidis (group B)
US-10-988-943-20
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; Publication No. US20050176085A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Neisseria meningitidis US-10-320-800-4
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                                 US-10-320-800-4
                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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Sequence 16, Application US/1098943
; Sequence 16, Application US/1098943
; Publication No. US20050176085A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE
; TITLE OF INVENTION: COMPLEX MIXTURES.
; TILE REPERENCE: Proceedies CU2003-269
; CURRENT PELLING DATE: 2004-11-15
; NUMBER OF SEQ ID NOS: 61
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121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 241;
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                                                                                                                                      Sequence 90, Application US/10467534
Publication No. US20040131625A1
GENERAL INPORMATION:
APPLICANT: Betthet, Yves
APPLICANT: Poolman, Jan
APPLICANT: Poolman, Jan
FILE REPRENCE: B455A1
CURRENT APPLICATION: Vaccine Composition
FILE REPRENCE: B455A1
CURRENT APPLICATION NUMBER: US/10/467,534
CURRENT FILING DATE: 2003-08-08
FRIOR FILING DATE: 2002-02-08
FRIOR FILING DATE: 2001-02-09
FRIOR APPLICATION NUMBER: GB 0103169.9
FRIOR RILING DATE: 2001-02-08
SOFTWARE: PARESE FOR FAILURG DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PARESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.7%; Score 206; DB 5; I 26.4%; Pred. No. 1.4e-13; atrive 30; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i LENGTH: 241
; TYPE: PRT
; ORGANISM: Neisseria meningitidis (group B)
US-10-988-943-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 26.4%,
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
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50 PTHENQLGAGAFGGYQVNPYVGFEMGYDWLGRMPYKGDNTNGAYKAQGVQLTAKLGYPIT 109
                                                                                                                                                                                                                                           95 SPVKPY--LGARL--SIARASVDIGGSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRY- 149
                                                                                                                                                                                                                                                                       49
                                                                                                                                            -----LRFAVDYTRYKNYKAPSTD--FKLYSIGASAIYDFDTQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-06

PRIOR PLING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PLING DATE: 2000-10-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-12-3

PRIOR PLING DATE: 2000-12-3

PRIOR PLING DATE: 2000-12-3

PRIOR PLING DATE: 2000-12-2

PRIOR PLING DATE: 2000-12-3

PRIOR PLING DATE: 2000-12-3

PRIOR PLING DATE: 2000-12-3

PRIOR PLING DATE: 2000-12-6

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16
                                                                                            1 MKKTAIAIAVALA------GFATVAQAAPKDNTWYAGAKLGWSQYHDTGFIHNDG
                                               1 MKK-ALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRIND-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
43;
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  85; Indels
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 69437, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Chery1
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlgen, Kari
                                                                                                                                                                                                                                                                                                                                                                         170 NNIGDANTIGTRPDNGLLSVGVSYRF 195
                                                                                                                                                                                                                                                                                                                                           150 NYIGKVNTV-KNVRSGELSVGVRVKF 174
  28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto, Robert
Forsyth, R.
Xu, H.
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Best Local Similarity 25.8%
Matches 54; Conservative
Conservative
                                                                                                                                               .---- 65
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     20;
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APPLICANT:
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APPLICANT:
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APPLICANT:
     Matches
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Rublication No. US20050186217A1

GENERAL INFORMATION:
APPLICANT:
MONDERLING, LAURA
APPLICANT:
MONDERLING, LAURA
TITLE OF INVERTION:
CURRENT APPLICATION NUMBER: US/10/946,647
CURRENT APPLICATION NUMBER: G0/504,119
PRIOR FILING DATE: 2003-09-19
PRIOR FILING DATE: 2003-09-19
NUMBER OF SEQ ID NOS: 1448
SOFTWARE: PALENTIN Version 3.3
SEQ ID NO 1377
LENGTH: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Publication No. US2005221439A1
GENERAL INFORMATION:
APPLICANT: BAXALETZ et al.
TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPEABLE H. INFLUENZAE
FILE REFERENCE: 28335/38815A
CURRENT APPLICATION NUMBER: US/10/795,159
CURRENT FILING DATE: 2004-03-05
PRIOR APPLICATION NUMBER: US 60/453,134
PRIOR FILING DATE: 2003-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 TQSPVKPYLGARLSLNRASVDLGG-----SDSFSQTSIGLGVLTGVSYAVTPNVDLD 144
                                                                                                      128 DKFDKFKPYIGARVAYGHVKHQVHSVRKETTTTFSPPAQGATVPGKIVQGPTNKPAYHES 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 VDYTRYKNY-----91
                                                                                                                                                                                                                                                                         123 ---TSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                   188 NSISSLGLGVIAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSLGMRYHF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 103.5; DB 5; Length 350; Pred. No. 0.026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Indels
                                                                                                                                                                        92 DTQSPVKPYLGARLSLNRA----SVDLGGSDSFSQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 14.1%; Score 122.5; DB 5
Best Local Similarity 33.3%; Pred. No. 3.8e-05;
Matches 30; Conservative 15; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 AGYRYNYIGKVNTVKNVRSGELSVGVRVKP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 LDYRYNDWGRLENVR-PKTHEASFGVRYRF 94
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 735, Application US/10795159
Publication No. US20050221439A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.9%;
24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 771
SOFWRARE: Patentin version 3.2
SEQ ID NO 735
LENGTH: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Salmonella enterica
US-10-946-647-1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: H. influenzae
US-10-795-159-735
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Best Local Similarity
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US-10-795-159-735
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Sequence 139, Application US/10732862A
; Sequence 139, Application W020040146524A1
; GENERAL INFORMATION:
    APPLICANT: ASHLEY, BIRKETT J.
    APPLICANT: Jay, Ratelynne J.
    TITLE OF INVENTION: STABILIZED IMMUNGENIC HBC CHIMER PARTICLES
    FILE REFRENCE: ICC-136.0 (4564-88881)
    CURRENT APLICANTON NUMBER: US/10/732,862A
    CURRENT PILING DATE: 2003-12-10
    FRIOR APPLICATION NUMBER: US 10/274,616
    FRIOR PILING DATE: 2002-10-21
    FRIOR FILING DATE: 2002-10-21
    FRIOR PILING DATE: 2002-02-21
    FRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.6%; Score 101; DB 4; Length 21; Best Local Similarity 100.0%; Pred. No. 0.001; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: January 11, 2006, 15:29:45 Job time : 116 secs
                              153 GKVNTVKNVRSGELSVGVRVK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 GKVNTVKNVRSGELSVGVRVK 173
                                                                1 GKVNTVKAVRSGELSVGVRVK 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-732-862A-139
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TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY
FILE REPERENCE: ICC-130.0 4564/85124

CURRENT APPLICATION NUMBER: 108/10/082,014

CURRENT FILING DATE: 2002-02-22

PRIOR APPLICATION NUMBER: 09/930,915

PRIOR APPLICATION NUMBER: 09/930,915

NUMBER OF SEQ ID NOS: 290

SOPTWARE: Patentin version 3.1

SEQ ID NO 124

LENGTH: 21
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APPLICANT: Priede, Mark
APPLICANT: Friede, Martin
TITLE OF INVENTION: STABLILEED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
TITLE OF INVENTION: CHRONIC HEPATITIS
FILE REPERENCE: 4564/87179
CURRENT APPLICATION NUMBER: 02(10/372,076
CURRENT FILING DATE: 2003-02-21
PRIOR PILING DATE: 2002-02-21
PRIOR PLICATION NUMBER: 10/080,299
PRIOR PILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 308
SOFTWARE PATENTIN OF SEQ ID NOS: 308
SOFTWARE PATENTIN OF SEQ ID NOS: 308
SOFTWARE PATENTIN OF SEQ ID NOS: 308
LENGTH: 21
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                                                                                                                                                                                                                                                                                                61 LDGDTQLGLTFAYMLTNHIGIELLAATPFNHTVSVKGLGPGLDGKLADVKHLPPTLSLQY 120
                                                                                                                                                                                                                                                89 YDFDTQSPVKPYLGARLS-----LNRASVDLGGSDSFSQTSIGLGVLTGVSYAVTPN 140
                                 1 MNKHILRASIAALATAPLAANAYEKGDFIVRAGAAHVQPNEDSGEVRLDGAKVSGTKST 60
                                                                                                                      57 ND-----LRFAVDYTRYKNYK-------ASAI 88
1 MKKAL--ATLIALAL--PAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRI 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                    141 VDLDAGYRYNYIGKVNTVKNVRSGELSVG 169
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-10-372-076-125
Sequence 125, Application US/10372076
Publication No. US20030198645A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-082-014-124
; Sequence 124, Application US/10082014
; Publication No. US20030185858A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 GKVNTVKNVRSGELSVGVRVK 173
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US-10-082-014-124
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; ORGANISM: Neisseria meningitidis
US-10-372-076-125
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Best Local S:
Matches 21
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Gaps

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Copyright (c) 1993 - 2006 Compugen Ltd.
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January 11, 2006, 15:22:23 ; Search time 29 Seconds (without alignments) 56.725 Million cell updates/sec US-10-650-123-2 868 1 MKKALATLIALALPAAALAE........VNTVKNVRSGELSVGVRVKF 174 Title: Perfect score: Sequence:

Scoring table:

67062 seqs, 9454214 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

67062 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Published Applications AA New:\*

1: /cgn2\_6/ptodata/2/pubpaa/USOB NEW PUB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/USOF NEW PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/USO7 NEW PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW PUB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/USO7 NEW PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/USIO\_NEW\_PUB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/USIO\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/USIO\_NEW\_PUB.pep:\* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	A Query Match	* Query Match Length DB	80	ID	Description
-	898	100.0	174	9	US-10-984-376-7	Sequence 7, Appli
~	862	99.3	174	9	US-10-984-376-8	Sequence 8, Appli
ო	852	98.2	174	9	US-10-984-376-10	10
4	852	98.2	174	9	US-10-984-376-11	Sequence 11, Appl
Ŋ	849	97.8	174	9	US-10-984-376-9	Sequence 9, Appli
9	846	97.5	174	9	US-10-984-376-12	Sequence 12, Appl
7	825	95.0	174	7	US-11-103-957-90	Sequence 90, Appl
60	809.5	93.3	175	9	US-10-467-657-2512	2512
0	805	92.7	174	9	US-10-984-376-14	
2	785.5	90.5	173	9	US-10-984-376-13	13,
1	224	25.8	232	9	US-10-467-657-5652	Sequence 5652, Ap
12	218.5	25.2	229	9	US-10-467-657-6238	
13	218	25.1	226	9	US-10-467-657-6038	Sequence 6038, Ap
14	214	24.7	281	9	US-10-467-657-8006	Sequence 8006, Ap
15	212	24.4	278	9	US-10-467-657-6726	
16	210	24.2	265	9	US-10-467-657-1778	
17	208	24.0	191	7	US-11-052-554A-86	
18	207.5	23.9	186	9	US-10-467-657-7854	Sequence 7854, Ap
19	206	23.7	278	9	US-10-467-657-7386	Sequence 7386, Ap
20	204.5	23.6	229	9	US-10-467-657-1754	Sequence 1754, Ap
21	194.5	22.4	227	9	US-10-467-657-54	Sequence 54, Appl
22	194.5	22.4	227	9	US-10-467-657-830	830
23	178	20.5	189	9	US-10-467-657-3184	Sequence 3184, Ap
24	94.5	10.9	212	7	US-11-052-554A-198	Sequence 198, App
52	88.5	10.2	703	7	US-11-052-554A-97	Sequence 97, Appl

Sequence 25, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 34, Appl Sequence 34, Appl Sequence 4, Appli Sequence 179, Appli Sequence 179, Appli Sequence 179, Appli Sequence 6, Appli	Sequence 2/04, Ap
US-11-103-957-25 US-11-052-554A-203 US-10-984-376-17 US-10-984-376-18 US-11-052-554A-39 US-11-052-554A-39 US-11-056-850-1 US-11-096-850-1 US-11-052-554A-179 US-11-052-554A-179 US-11-052-554A-62 US-11-052-554A-63 US-11-052-554A-64 US-11-052-554A-64 US-11-052-554A-64 US-11-052-554A-64 US-11-052-554A-64 US-11-052-554A-64 US-11-052-554A-64 US-11-052-554A-64 US-11-052-554A-64	US-11-052-554A-142
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87.5 81.5 77 72.5 72.5 72.5 71.7 71.7 70.5 69.5	69.5
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## ALIGNMENTS

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TYPE: PRT
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| Publication No. US20050244436A1
| GENERAL INFORMATION:
| APPLICANT: GIULIANI, Marzia Monica
| APPLICANT: PIZZA, Mariagrazia
| APPLICANT: RAPPUOLI, Rino
| TILLE OF INVERTION: COMBINATION NUMBER: US/10/984,376
| CURRENT FILING DATE: 2004-11-09
| PRIOR PILING DATE: 2001-11-19
| PRIOR PILING DATE: 1999-05-19
| PRIOR PILING DATE: 1999-05-19
| PRIOR PILING DATE: 1999-05-19
| PRIOR PILING DATE: 1999-06-19
                                                                                                                APPLICANT: GAUGLANI, MATELA TOLLICA
APPLICANT: FIZZA, MATELAGIZA
APPLICANT: RAPPUOLI, Rino
TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
FILE REFERENCE: 2300-1609.20
CURRENT APPLICATION NUMBER: US/10/984,376
CURRENT APPLICATION NUMBER: 09/979,263
PRIOR APPLICATION NUMBER: 09/979,263
PRIOR APPLICATION NUMBER: 09/979,263
PRIOR APPLICATION NUMBER: 6B 9911692.3
PRIOR APPLICATION NUMBER: GB 9911692.3
PRIOR PILING DATE: 1999-05-19
PRIOR PLING DATE: 1999-06-19
PRIOR PLING DATE: 1999-08-19
Sequence 8, Application US/10984376; Publication No. US20050244436A1; GENERAL INFORMATION: APPLICANT: GIULIANI, Marzia Monica
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NUMBER OF SEQ ID NOS: 18
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US-10-984-376-8
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ORGANISM: Artificial
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61 PAVDYTRYKNYKAPSTDPKLYSIGASAIYDPDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                                                                                                                                                                                                                                                                                              Query Match 98.2%; Score 852; DB 6; Length 174; Best Local Similarity 98.3%; Pred. No. 2e-77; Matches 171; Conservative 1; Mismatches 2; Indels
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| Sequence 11, Application US/10984376
| Publication No. US20050244436A1
| GENERAL INFORMATION:
| APPLICANT: GIULIANI, Marzia Monica
| APPLICANT: RAPPUOLI, Rino
| TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
| TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
| FILE REFERENCE: 2300-1609-20
| CURRENT APPLICATION NUMBER: US/10/984,376
| CURRENT FILING DATE: 2001-11-19
| PRIOR APPLICATION NUMBER: PCT/IB00/00828
| PRIOR PILING DATE: 2001-01-19
| PRIOR FILING DATE: 1999-05-19
| PRIOR FILING DATE: 1999-05-19
| PRIOR FILING DATE: 1999-05-19
| PRIOR FILING DATE: 1999-06-19
SOFTWARE: PatentIn version 3.3 SEQ ID NO 10 LENGTH: 174
                                                                                                                               ) ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NSPA
US-10-984-376-10
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US-10-984-376-11
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, ORGANISM: Neisseria gonorrhoeae
US-11-103-957-90
NUMBER OF SEQ ID NOS: 18
SOFWHARB: Patentin version 3.3
SEQ ID NO 12
LENGTH: 174
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Best Local Similarity 97.7%;
Matches 170; Conservative
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COTHER INFORMATION: NSPA
US-10-984-376-12
                                                                                       TYPE: PRT
ORGANISM: Artificial
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US-10-467-657-2512
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                                                                                                                                           GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: PIZZA, MATISARAL

APPLICANT: PIZZA, MATISARAL

APPLICANT: PIZZA, MATISARAL

TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS:

TITLE OF INVENTION: COMBINATION NEISSERIAL

CURRENT APPLICATION NUMBER: US/10/984,376

CURRENT APPLICATION NUMBER: 09/979,263

PRIOR APPLICATION NUMBER: 09/979,263

PRIOR APPLICATION NUMBER: PCT/1B00/00828

PRIOR APPLICATION NUMBER: GB 9911692.3

PRIOR PILING DATE: 1999-05-19

PRIOR FILING DATE: 1999-05-19

PRIOR FILING DATE: 1999-06-19

PRIOR FILING DATE: 1999-06-19

PRIOR FILING DATE: 1999-08-19

PRIOR FILING DATE: 1999-08-19

PRIOR PILING DATE: 1999-08-19

PRIOR PILING DATE: 1000-03-09

NUMBER OF EQ ID NOS: 18

SEQ ID NO 9

LENGTH: 174

MUNDER OF EXCENTION NUMBER: GB DATE: 1000-03-09

NUMBER OF EXCENTION NUMBER: GB DATE: 1000-03-09

SEQ ID NO 9
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| Publication No. US20050244436A1
| GENERAL INPORMATION:
| APPLICANT: GIULIANI, Marzia Monica
| APPLICANT: GILLANI, Marzia Monica
| APPLICANT: GILLANI, Mariagrazia
| APPLICANT: RAPPUCLI, Rino
| TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
| FILE REFERENCE: 2300-1609_20
| CURRENT APPLICATION NUMBER: US/10/984,376
| CURRENT FILING DATE: 2004-11-09
| PRIOR FILING DATE: 2001-11-19
| PRIOR PLICATION NUMBER: PCT/IB00/00828
| PRIOR PLICATION NUMBER: PCT/IB00/00828
| PRIOR PLILING DATE: 1999-05-19
| PRIOR PLILING DATE: 1999-05-19
| PRIOR PLILING DATE: 1999-05-19
| PRIOR PLILING DATE: 1999-06-19
| PRIOR PLILING DATE: 2000-03-09
| PRIOR PLILING DATE: 2000-03-09
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98.3%; Pred. No. 3.9e-77;
tive 0; Mismatches 3.
                                                                    US-10-984-376-9

Sequence 9, Application US/10984376
; Publication No. US20050244436A1
; GENERAL INFORMATION:
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ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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US-10-984-376-12
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61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120 120 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120 61 FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF 120 9 9 1 MKKALATLIALAIPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDIR 60 1 MKKALAALIALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR Gaps Gaps 121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174 121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174 ; 0 ö Query Match 95.0%; Score 825; DB 7; Length 174; Best Local Similarity 94.3%; Pred. No. 9.2e-75; Matches 164; Conservative 2; Mismatches 8; Indels Score 846; DB 6; Length 174; Pred. No. 7.8e-77; 1; Mismatches 3; Indels Sequence 90, Application US/11103957

Sequence 90, Application US/11103957

Publication No. US20050281847A1

GENERAL INFORMATION:

APPLICANT: Berthet, Francois-Xavier Jacques

APPLICANT: Lobet, Yoes

APPLICANT: Veclman, Jan

APPLICANT: Veclman, Vincent Georges Christian Louis

FILE REFERENCE: 145.261

CURRENT APPLICATION NUMBER: US/11/103,957

CURRENT APPLICATION NUMBER: US/10/467,534

PRIOR APPLICATION NUMBER: US/10/467,534

PRIOR APPLICATION NUMBER: GB 0103169.9

PRIOR FILING DATE: 2004-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2004-02-08

PRIOR FILING DATE: 2004-02-08

PRIOR FILING DATE: 2004-02-08

PRIOR FILING DATE: 2004-02-08

PRIOR FILING DATE: 2004-02

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US-10-984-376-14

Sequence 14, Application US/10884376

Publication No. US20050244436A1

GENERAL INFORMATION:
APPLICANT: GILLANI, Marzia Monica
APPLICANT: PIZZA, Mariagrazia
APPLICANT: RAPPUCLI, Rino
TILE OF INVERTY EMPLICATION: COMBINATION NEISSERIAL COMPOSITIONS
FILE REFERENCE: 2300-1609.20
CURRENT FILING DATE: 2004-11-09
PRIOR PRILICATION NUMBER: US/979,263
PRIOR APPLICATION NUMBER: PCT/IB00/00828
PRIOR PLICATION NUMBER: GB 9911692.3
PRIOR PLICATION NUMBER: GB 9911692.3
PRIOR FILING DATE: 1999-05-19
PRIOR PLICATION NUMBER: GB 9919705.5
PRIOR FILING DATE: 1999-06-19
PRIOR FILING DATE: 1999-06-19
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.3
SOFTWARE: Patentin version 3.3
                                                                APPLICANT: CHIRON SpA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: PLAZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Blisabetta
APPLICANT: WONACI BLISABORTS
APPLICANTON: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 2512
Sequence 2512, Application US/10467657
Publication No. US20050260581A1
                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2512
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US-10-984-376-14
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                       Publication No. US20
GENERAL INFORMATION:
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Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/10984376

Sequence 13, Application US/10984376

Publication NO.

APPLICANT: GIULIANI, Marzia Monica

APPLICANT: BIZZA, Marzia Monica

APPLICANT: RAPPULI, Rino

TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS

FILE REFREENCE: 2300-1609.20

CURRENT APPLICATION NUMBER: US/10/984,376

CURRENT PILING DATE: 2004-11-09

PRIOR FILING DATE: 2001-11-19

PRIOR FLING DATE: 2001-11-19

PRIOR FLING DATE: 2001-05-19

PRIOR PLING DATE: 1999-06-19

PRIOR PLING DATE: 1999-06-19

PRIOR PLING DATE: 1999-06-19

PRIOR PLING DATE: 1999-06-19

PRIOR PLING DATE: 2000-03-09

NUMBER: OF SEQ ID NOS: 18

SOFTWARE: PATENTIN NUMBER: GB 9919705.5

PRIOR PLING DATE: 2000-03-09

SEQ ID NO 13

LENGTH: 173

"WHICH IN THE PATENTIN NUMBER: GB 0005730.7

PRIOR PLING DATE: 2000-03-09

SEQ ID NO 13

LENGTH: 173
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9; Indels
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90.5%; Score 785.5; DB 6
Best Local Similarity 93.1%; Pred. No. 7.3e-71;
Matches 162; Conservative 1; Mismatches 10
  1; Mismatches
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GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: CHIRON SpA
APPLICANT: PIZZA MARIAGIZA
APPLICANT: PIZZA MARIAGIZA
APPLICANT: MASIGNANI Vega
  Matches 164; Conservative
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US-10-984-376-13
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US-10-467-657-6038
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                                                                                                                                                                                                                                                  Length 232;
                                                                                                                                                                                                                                                                                 53; Indels
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APPLICANT: PONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Blisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE:
 TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS FILE REFERENCE:
                                                                                                                                                                                                                                               ; Score 224; DB 6; ; Pred. No. 3.1e-15; 30; Mismatches 53;
                                         CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR PILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTHARE: SeqWin99, version 1.04
SEQ ID NO 5652
LENGTH: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SEQ ID NO 6238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6238, Application US/10467657
Publication No. US20050260581A1
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                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5652
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ORGANISM: Neisseria gonorrhoeae
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APPLICANT: MONACI Elisabetta
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Best Local Similarity
Matches 64; Conserva
                                                                                                                                                                                                                                                                Similarity
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Best Local 3
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                                                                                    125 IGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVERTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REPRENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT PILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR APPLICATION NUMBER: 2001-02.12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqMin99, version 1.04
SEQ ID NO 8006
LENGTH: 281
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CHILDON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: POSTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGRANI Vega
APPLICANT: MASIGRANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR PILING DATE: 2001-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.1%; Score 218; DB 6; Best Local Similarity 28.1%; Pred. No. 1.2e-14; Matches 59; Conservative 28; Mismatches 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 AGYRYNYIGKVNTVKNVRSGBLSVGVRVKF 174
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198 TGYRYHNWGRLENTR-FKTHEASLGVRYRF 226
                                                                                                                                                                                                                                                                            ; Sequence 6038, Application US/10467657; Publication No. US20050260581A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8006, Application US/10467657 Publication No. US20050260581A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 6038
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                                                                                                                                                                                                                                                                                                                                     77 DFK------ASYDIGASALYDFDTQSPVKPYLGARLSLNR------ASYDLGGS 117
                                                                                                                                                                                                                                                                                                                                                                118 DSFSQTSI------GLGVLTGVSYAVTPNVDLDAGYRYNYIGKNNTV 158
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202 GTKPTYYDDIDSGKNQKNTYRQNRSSRRLGFGAMAGVGIDVAPGLTLDAGYRYHYWGRLE 261
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207 DGSAKTSVPSEMPPKPAYHENRSSRRLGFGAMAGVGIDVAPGLTLDAGYRYHYWGRLENT 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 SLLFSSAARAGEDHGRGPYVQADLAYAYEHITRDYPDAAGANKGKISTVSDYFRNIRTH 81
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                                                                                                                                                                     10 ALALPAAALAEG---ASGPYVQADAAHA------KASSSLGS-----A 43
                                                                                                                             Gaps
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                                                                               Query Match 24.7%; Score 214; DB 6; Length 281; Best Local Similarity 25.4%; Pred. No. 4e-14; Matches 65; Conservative 31; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CHIRON SpA
APPLICANT: CHIRON SpA
APPLICANT: PONTANA Maria Rita
APPLICANT: PLIZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
ITITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 200-212
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SegWin99, version 1.04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6726, Application US/10467657; Publication No. US20050260581A1; GENERAL INFORMATION:
  ; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8006
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ORGANISM: Neisseria gonorrhoeae
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267 R-FKTHEASLGVRYRF 281
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US-10-467-657-6726
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LENGTH: 278
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TYPE: PRT
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Qy 157 TVKNVRSGELSVGVRVKF 174

Db 262 NTR-FKTHEASLGVRYRF 278

Search completed: January 11, 2006, 15:30:26 Job time : 30 secs